GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:14 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1637	100.0	310	9	US-09-909-320-423	Sequence 423, App
2	1637	100.0	310	9	US-09-909-088B-423	Sequence 423, App
3	1637	100.0	310	9	US-09-905-291A-423	Sequence 423, App
4	1637	100.0	310	9	US-09-902-853-423	Sequence 423, App
5	1637	100.0	310	9	US-09-907-824-423	Sequence 423, App
6	1637	100.0	310	9	US-09-907-841-423	Sequence 423, App
7	1637	100.0	310	10	US-09-904-011-423	Sequence 423, App
8	1637	100.0	310	10	US-09-906-742-423	Sequence 423, App
9	1637	100.0	310	10	US-09-906-838-423	Sequence 423, App
10	1637	100.0	310	10	US-09-907-613-423	Sequence 423, App
11	1637	100.0	310	10	US-09-907-942-423	Sequence 423, App
12	1637	100.0	310	10	US-09-904-859-423	Sequence 423, App
13	1637	100.0	310	10	US-09-909-204-423	Sequence 423, App
14	1637	100.0	310	10	US-09-904-820-423	Sequence 423, App
15	1637	100.0	310	10	US-09-904-786-423	Sequence 423, App
16	1637	100.0	310	10	US-09-906-646-423	Sequence 423, App
17	1637	100.0	310	10	US-09-906-700-423	Sequence 423, App
18	1637	100.0	310	10	US-09-903-786-423	Sequence 423, App
19	1637	100.0	310	10	US-09-902-903-423	Sequence 423, App
20	1637	100.0	310	10	US-09-903-749A-423	Sequence 423, App
21	1637	100.0	310	10	US-09-904-119-423	Sequence 423, App
22	1637	100.0	310	10	US-09-904-956-423	Sequence 423, App
23	1637	100.0	310	10	US-09-902-736-423	Sequence 423, App
24	1637	100.0	310	10	US-09-907-794-423	Sequence 423, App
25	1637	100.0	310	10	US-09-903-943-423	Sequence 423, App
26	1637	100.0	310	10	US-09-904-462-423	Sequence 423, App
27	1637	100.0	310	10	US-09-907-925-423	Sequence 423, App
28	1637	100.0	310	10	US-09-902-692-423	Sequence 423, App
29	1637	100.0	310	10	US-09-903-520-423	Sequence 423, App
30	1637	100.0	310	10	US-09-905-056-423	Sequence 423, App
31	1637	100.0	310	10	US-09-909-064-423	Sequence 423, App
32	1637	100.0	310	10	US-09-904-553-423	Sequence 423, App
33	1637	100.0	310	10	US-09-905-381-423	Sequence 423, App
34	1637	100.0	310	10	US-09-905-088-423	Sequence 423, App
35	1637	100.0	310	10	US-09-907-575-423	Sequence 423, App
36	1637	100.0	310	10	US-09-905-075-423	Sequence 423, App
37	1637	100.0	310	10	US-09-902-759-423	Sequence 423, App
38	1637	100.0	310	10	US-09-902-634-423	Sequence 423, App
39	1637	100.0	310	10	US-09-902-713-423	Sequence 423, App
40	1637	100.0	310	10	US-09-907-979-423	Sequence 423, App
41	1637	100.0	310	10	US-09-902-615-423	Sequence 423, App
42	1637	100.0	310	10	US-09-903-925-423	Sequence 423, App
43	1637	100.0	310	10	US-09-906-760A-423	Sequence 423, App
44	1637	100.0	310	10	US-09-903-823-423	Sequence 423, App
45	1637	100.0	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

```
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-320-423

  Query Match           100.0%;  Score 1637;  DB 9;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,088B
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-088B-423

  Query Match           100.0%;  Score 1637;  DB 9;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 3
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,291A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-291A-423

  Query Match             100.0%;  Score 1637;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-841-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011

; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien

US-09-904-011-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 8
US-09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

```
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-742-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 9
US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Baton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,838
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-838-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 10
US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,613
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-613-423

  Query Match           100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 11
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

```
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-859-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,204
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-204-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 14
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Désnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,820
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-820-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
US-09-904-786-423
; Sequence 423, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
```

```
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,786
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-786-423

  Query Match             100.0%;  Score 1637;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: June 15, 2004, 11:08:02
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:59:09 ; Search time 14.5 Seconds
(without alignments)
2056.508 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	424	25.9	299	2	S56749	junctional adhesio
2	187	11.4	725	2	JE0099	neural cell adhesi
3	186	11.4	1088	1	IJXLNL	neural cell adhesi
4	180.5	11.0	1894	2	C54689	protein-tyrosine-p
5	177	10.8	725	2	JE0100	neural cell adhesi
6	177	10.8	1092	1	JN0635	neural cell adhesi
7	174	10.6	333	2	A31923	amalgam protein pr
8	171.5	10.5	725	1	IJMSNG	neural cell adhesi
9	171.5	10.5	1115	1	IJMSNL	neural cell adhesi
10	169.5	10.4	858	1	IJRTNC	neural cell adhesi
11	169.5	10.4	1912	2	A56178	protein-tyrosine-p
12	164.5	10.0	3707	2	S18252	heparan sulfate pr
13	163.5	10.0	1051	2	A39712	kinase-like protei
14	161.5	9.9	853	1	IJBONC	neural cell adhesi
15	161	9.8	538	2	JC2457	vascular cell adhe
16	161	9.8	1091	1	IJCHNL	neural cell adhesi
17	160.5	9.8	761	1	IJHUNG	neural cell adhesi
18	160.5	9.8	1612	2	T30805	dutt1 protein - mo
19	160	9.8	7962	2	I38346	elastic titin - hu
20	159.5	9.7	1033	2	S19247	cell adhesion prot
21	159.5	9.7	6642	2	T29757	protein UNC-89 - C
22	159	9.7	1323	2	PN0568	connectin 3B - chi
23	159	9.7	4162	2	T42633	connectin/titin -
24	155.5	9.5	1259	2	A43425	Bravo/Nr-CAM cell
25	155.5	9.5	1268	1	A39640	neural cell adhesi
26	155	9.5	344	2	I56551	neurotrimin - rat
27	155	9.5	1907	2	S50893	protein-tyrosine-p
28	154.5	9.4	495	2	T25750	hypothetical prote
29	154	9.4	1501	2	I58148	protein-tyrosine-p
30	154	9.4	1863	2	S46217	protein-tyrosine-p
31	153	9.3	352	2	T33433	hypothetical prote
32	153	9.3	875	2	T33434	hypothetical prote
33	152	9.3	483	2	T17346	hypothetical prote
34	150.5	9.2	365	2	JC7780	coxsackie- and ade
35	150.5	9.2	702	2	A36319	carcinoembryonic a
36	150	9.2	1651	2	T14160	transmembrane rece
37	149	9.1	521	2	S34338	biliary glycoprote
38	148	9.0	1262	1	B48758	protein-tyrosine-p
39	148	9.0	1496	1	A48758	protein-tyrosine-p
40	147.5	9.0	871	1	I48696	protein-tyrosine k
41	147.5	9.0	881	1	I48697	protein-tyrosine k
42	147.5	9.0	1897	1	TDHULK	leukocyte antigen-
43	147	9.0	1898	2	S46216	leukocyte antigen-
44	146.5	8.9	423	2	T29549	hypothetical prote
45	146.5	8.9	458	2	JC1509	biliary glycoprote

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 25.9%; Score 424; DB 2; Length 299;
Best Local Similarity 32.8%; Pred. No. 1.4e-27;
Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

```
Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              | | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
                | |||: ||  || |||  :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    |  |                ||:|
```

```
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299
```

RESULT 2
JE0099
neural cell adhesion molecule 1 - African clawed frog
N;Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match   11.4%; Score 187; DB 2; Length 725;
  Best Local Similarity   28.9%; Pred. No. 1.6e-07;
  Matches   61; Conservative   30; Mismatches   84; Indels   36; Gaps   11;

```
Qy         30 GAVNLK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||     :    |  |||:  | : || |  :| |  | |: | :|      | |
Db        105 GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
              :      |  :|    |:|  : : |   ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHL 197
              : :    ||     : :   | | :::| | |  || :   |:
Db        214 RQL----RVNATAKMAESVVLSC-DADGFPDPEISWLKKGEPIEDG--------EEKISF 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :    | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291
```

RESULT 3
IJXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <I
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pr
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match   11.4%; Score 186; DB 1; Length 1088;
  Best Local Similarity   28.9%; Pred. No. 3.2e-07;
  Matches   61; Conservative   30; Mismatches   84; Indels   36; Gaps   11;

```
Qy         30 GAVNLK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||     :    |  |||:  | : || |  :| |  | |: | :|      | |
Db        105 GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
              :      |  :|    |:|  : : |   ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHL 197
              : :    ||     : :   | | :::| | |  || :   |:
Db        214 RQL----RVNATANMAESVVLSC-DADGFPDPEISWLKKGEPIEDG--------EEKISF 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :    | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291
```

RESULT 4
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precurso
N;Alternate names: MPTP delta type B/C
N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C;Accession: C54689; B54689
R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specializ
A;Reference number: A54689; MUID:93360986; PMID:8355697
A;Accession: C54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1894 <MIZ>
A;Experimental source: brain; splice form B
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)
A;Accession: B54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
A;Experimental source: brain; splice form C
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy
F;45-107/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;317-399/Domain: fibronectin type III repeat homology <FN3A>
F;1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted

```
F;1542/Binding site: substrate phosphate (Arg) #status predicted
F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1832/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             11.0%;  Score 180.5;  DB 2;  Length 1894;
  Best Local Similarity   28.8%;  Pred. No. 1.8e-06;
  Matches   72;  Conservative   34;  Mismatches   75;  Indels   69;  Gaps   15;

Qy          3 LRRPPRLRL------CARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIIT 56
              :|||  | |       ||  |  |                      ||||  |   |  ::  |
Db         11 VRRPLSLLLTPFLCACAETPPRF-----------------TRTPVDQTGVSGGVASFIC 52

Qy         57 DSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDS 110
               : | |||   | |    ||: :::   : ||:       |   :|    |:    | ||
Db         53 QA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSGSVLRIQPLR----TPRDE 100

Qy        111 ALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKM-----------ATL 158
              |:|  |  || |:  ||  :   |||  :      ::|:  |   |             ||:
Db        101 AIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPTIDMGPQLKVVERTRTATM 152

Qy        159 HCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSET-GTLVFTAVHKDDSGQY 217
              |  | |:| |  :|::: :|: | |  | | :     | ||: | |       : | |:|
Db        153 LCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSESIGALQIEQSEESDQGKY 206

Qy        218 YCIASNDAGS 227
              |:|:| ||:
Db        207 ECVATNSAGT 216


RESULT 5
JE0100
neural cell adhesion molecule 2 - African clawed frog
N;Alternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0100
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0100
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BAA25932.1; PID:g3116229
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match             10.8%;  Score 177;  DB 2;  Length 725;
  Best Local Similarity   28.6%;  Pred. No. 1.1e-06;
  Matches   60;  Conservative   28;  Mismatches   88;  Indels   34;  Gaps   10;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||   :       |  |||   | : || |  :| |  | |: | :|     | |
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
               :       |  :|    |:|  : : |   ||||  ::||    ||:   |:: | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLN 198
                  ||    : :   | | :::| | |  || :   |:                   |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDG--------EEKISFN 261

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
               :   :    | |:|  :| |||:| || |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 6
JN0635
neural cell adhesion molecule 2 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C;Accession: JN0635
R;Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993
A;Title: Two neural-cell adhesion molecule(NCAM)-encoding genes in Xenopus laevis are e
A;Reference number: JN0635; MUID:93273239; PMID:7684721
A;Accession: JN0635
A;Molecule type: mRNA
A;Residues: 1-1092 <TON>
A;Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
C;Genetics:
A;Gene: NCAM2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialogly
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;317-381/Domain: immunoglobulin homology <IMM3>
F;413-475/Domain: immunoglobulin homology <IMM4>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;619-680/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1092/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.8%;  Score 177;  DB 1;  Length 1092;
  Best Local Similarity   28.6%;  Pred. No. 1.8e-06;
  Matches   60;  Conservative   28;  Mismatches   88;  Indels   34;  Gaps   10;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||   :       |  |||   | : || |  :| |  | |: | :|     | |
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
               :       |  :|    |:|  : : |   ||||  ::||    ||:   |:: | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLN 198
                  ||    : :   | | :::| | |  || :   |:                   |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDG--------EEKISFN 261

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
               :   :    | |:|  :| |||:| || |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 7
A31923
amalgam protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D
A;Reference number: A31923; MUID:89028670; PMID:3141062
A;Accession: A31923
A;Molecule type: DNA
A;Residues: 1-333 <SEE>
A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C;Genetics:
A;Gene: FlyBase:Ama
A;Cross-references: FlyBase:FBgn0000071

  Query Match             10.6%;  Score 174;  DB 2;  Length 333;
```

```
  Best Local Similarity   26.3%;  Pred. No. 7.7e-07;
  Matches   51;  Conservative   39;  Mismatches   84;  Indels   20;  Gaps    5;

Qy         35 KSSNRTPVVQEPESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEI 94
              ::: :: :| | :::||:|    :    | | | :           :    :     :
Db        143 ENTPKSTLVTEGQNLELTC--HANGFPKPTISWAR------------EHNAVMPAGGHL 187

Qy         95 LGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGK 154
              | : :|:| :| | |    | |  :|:|   : |: :| : |: :|   | |   | |
Db        188 LAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSH 245

Qy        155 MATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDS 214
              | | |   :|:| |   |::| |||   |  :    |::   : | |  :| ::|
Db        246 SAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEEDF 302

Qy        215 GQYYCIASNDAGSA 228
              | ||| |:|  | |
Db        303 GDYYCNATNKLGHA 316


RESULT 8
IJMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N;Alternate names: NCAM-120
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00382; A44290
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-725 <BAR>
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00382
A;Molecule type: DNA
A;Residues: 642-656,'D',658-725 <BA2>
A;Cross-references: EMBL:X07195
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 701/1
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.5%;  Score 171.5;  DB 1;  Length 725;

  Best Local Similarity   27.3%;  Pred. No. 3.1e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEPESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIPQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                    :   |  :: |:  |  :|     |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RPIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |:: | | |      :  |      :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEB-D 260

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
              | |:|     |::  :     | |:|  :| ||| | ||      ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 9
IJMSNL
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00844; S00384; A28281; A44290; S00383
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonte
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,0(
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,'1
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse ne
A;Reference number: S00844; MUID:88067687; PMID:3684567
A;Accession: S00844
A;Molecule type: mRNA
A;Residues: 529-809,1077-1115 <SAN>
A;Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
R;Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJ
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
```

```
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TMM>
F;730-1115/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.5%;  Score 171.5;  DB 1;  Length 1115;
  Best Local Similarity   27.3%;  Pred. No. 5.2e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
                |:: |          ||:|   :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                  :   |  :: |:  |  :|    |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                |:: | | |     :  |     :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                | |:|     |::  :    | |:|  :| ||| | ||     ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 10
IJRTNC
neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence for a
A;Reference number: S00846; MUID:88059265; PMID:3680385
A;Accession: S00846
A;Molecule type: mRNA
A;Residues: 1-858 <SMA>
A;Cross-references: EMBL:X06564
R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-364 <RES>
A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <M
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMM4>
F;430-492/Domain: immunoglobulin homology <IMM5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TMM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 858;
  Best Local Similarity   26.3%;  Pred. No. 5.6e-06;
  Matches   61;  Conservative   42;  Mismatches   84;  Indels   45;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
                |:: |          ||:|   :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                  :   |  :: |:  |  :|    |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                |:: | | |     :  |     :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEEDD 261

Qy        188 PRFRNSSFHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                :      |: : ::  |     | |:|  :| ||| | ||     ||:  ::
Db        262 EK------HIFSDDSSELTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 11
A56178
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
N;Alternate names: protein-tyrosine-phosphatase BPTP-2
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56178; S12052; B44929
R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A;Title: Molecular characterization of the human transmembrane protein-tyrosine phospha
ase delta isoforms.
A;Reference number: A56178; MUID:95204468; PMID:7896816
A;Accession: A56178
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1912 <PUL>
A;Cross-references: GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
R;Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A;Title: Structural diversity and evolution of human receptor-like protein tyrosine pho
A;Reference number: S12049; MUID:91006018; PMID:2170109
A;Accession: S12052
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 390-1912 <KRU>
A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-
```

```
R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancer Res. 52, 737-740, 1992
A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A;Reference number: A44929; MUID:92119637; PMID:1370651
A;Accession: B44929
A;Molecule type: mRNA
A;Residues: 1756-1804,'C',1806-1845 <ADA>
A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
A;Experimental source: pre-B cell NALM-6
A;Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
C;Genetics:
A;Gene: GDB:PTPRD
A;Cross-references: GDB:131384; OMIM:601598
A;Map position: 9p24-9p24
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;38-100/Domain: immunoglobulin homology <IMM1>
F;140-209/Domain: immunoglobulin homology <IMM2>
F;250-304/Domain: immunoglobulin homology <IMM3>
F;711-811/Domain: fibronectin type III repeat homology <3FR>
F;1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1559/Binding site: substrate phosphate (Arg) #status predicted
F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1850/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             10.4%;  Score 169.5;  DB 2;  Length 1912;
  Best Local Similarity   28.6%;  Pred. No. 1.5e-05;
  Matches   65;  Conservative   35;  Mismatches   76;  Indels   51;  Gaps   13;

Qy         39 RTPVVQEFESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRA 92
              |||| |    |  ::  |  : | |||  | |    ||: :::   : ||:       |
Db         28 RTPVDQTGVSGGVASFICQA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSG 79

Qy         93 EILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV 152
              :|    |:    | || |:| |  || |:  ||  :   |||  :      ::|:  |
Db         80 SVLRIQPLR----TPRDEAIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPT 127

Qy        153 GKM------------ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSE 200
                |              ||: |  | |:| |  :|::: :|: | |  | | :     | ||
Db        128 IDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSE 181

Qy        201 T-------GTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMEVYDL 240
              :       | |      : | |:| |:|:| ||:       : | :|
Db        182 SIGGTPIRGALQIEQSEESDQGKYECVATNSAGTRYSAPANLYVREL 228


RESULT 12
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogl
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a gl
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G re
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicte

  Query Match             10.0%;  Score 164.5;  DB 2;  Length 3707;
  Best Local Similarity   27.0%;  Pred. No. 8.3e-05;
  Matches   63;  Conservative   35;  Mismatches   74;  Indels   61;  Gaps   13;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              :::  || : :   ||:            | |::|          : : | || :
Db       2428 LSVHGPPTVSV---LPE-----------GPVHVKMG---------KDITLECISSGEPR 2463

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              | ||  |         | :    |::  : |          ||| :|   |:  | |:  |:
Db       2464 SSPR--W--------TRLGIPVKLEPRMFGLMN--SHAMLKIASVKPSDAGTYVCQ--AQ 2509

Qy        121 N----DRKEIDEIVIELTVQVKPVTPVCRVPKA---VPVGKMATLHCQESEGHPRPHYSW 173
              |     :|:: |:::: |  | | ||  :| ::   :  |  |||||  : |:| |    |
Db       2510 NALGTAQKQV-ELIVD-TGTVAPGTPQVQVEESELTLEAGHTATLHC-SATGNPPPTIHW 2566

Qy        174 YRNDVPLPTDSRANPRFRNSSPHLNSETGTLVFTAVHKDDSGQYYCIASNDAG 226
              :  |||  |                 |  |||    | : |||| | |:| ||
Db       2567 SKLRAPLPWQHRI-------------EGNTLVIPRVAQQDSGQYICNATNSAG 2606


RESULT 13
A39712
kinase-like protein klg precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C;Accession: A39712
R;Chou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A;Title: Characterization of a member of the immunoglobulin gene superfamily that possi
A;Reference number: A39712; MUID:91271300; PMID:1711213
A;Accession: A39712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1051 <CHO>
A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C;Keywords: ATP
F;775-1046/Domain: protein kinase homology <KIN>
F;783-791/Region: protein kinase ATP-binding motif

  Query Match             10.0%;  Score 163.5;  DB 2;  Length 1051;
  Best Local Similarity   24.5%;  Pred. No. 2.2e-05;
  Matches   66;  Conservative   34;  Mismatches  110;  Indels   59;  Gaps   11;

Qy         40 TPVVQEFESVE------LSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAE 93
```

```
                 ||  |  : :|      :||  |  :   | |:| |           : :   :: ||
Db        486 TPPPQPLQCMEFNKEVTVSCSATGRE--KPTIQWTKTD---------GSSLPSHVSHRAG 534

Qy         94 ILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVG 153
               |     |:| ||  | |  :| |  :       ::| | |     :   |  |  |
Db        535 I-----LSFHKVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVYVTFKLEPEPTTVYQG 587

Qy        154 KMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDD 213
                 |   || :|| | ||  |  .  |   |:  || :          |:||   |  :|
Db        588 HTAMPQCQ-AEGDPVPHIQWKGKDKIL-DPSKLLPRIQ------IMPNGSLVIYDVTTED 639

Qy        214 SGQYYCIASNDAG-----------SARCEEQE----------MEVYDLNIGGIIGGVLV 251
                 ||:| |||  |                    || |          ::   |::|  :  :::
Db        640 SGKYTCIAGNSCNIKHREAPLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIII 699

Qy        252 VLAVLALITLGICCAYRRGYFINNKQDGE 280
                 ||  ::      |  |:  :   :||
Db        700 VLGLMF-----YCKKRRKAKRLKKHPEGE 723


RESULT 14
IJBONC
neural cell adhesion molecule short domain form precursor - bovine
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A;Reference number: A32976; MUID:89378239; PMID:2776887
A;Accession: A32976
A;Molecule type: mRNA
A;Residues: 1-853 <LIP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
A;Molecule type: protein
A;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A;Note: the authors identified this protein as calmodulin-independent adenylate cyclase
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: B44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Note: 23-Glu was also found
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F;20-719/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-288/Domain: immunoglobulin homology <IMM3>
F;261-270/Region: NCAM binding #status predicted
F;321-396/Domain: immunoglobulin homology <IMM4>
F;428-490/Domain: immunoglobulin homology <IMM5>
F;527-604/Domain: fibronectin type III repeat homology <FN3A>
F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transmembrane #status predicted <TMM>
F;738-853/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             9.9%;  Score 161.5;  DB 1;  Length 853;
  Best Local Similarity   26.0%;  Pred. No. 2.6e-05;
  Matches   60;  Conservative   38;  Mismatches   88;  Indels   45;  Gaps   11;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
               |:: |          ||:|   :       |  |||    | : |: |  :|  | | ||
Db         96 CVVTAEDGTESEATVNVKIFQKLMFKNAPTPQEFREGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                    :   |  :: |:  |  :|     |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLTNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |:: | | |      :  |      :|:  || |  :|| | |  || ::   :  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-NAEGFPEPTVSWTKDGEQIENE---- 257

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                 :  :  : ::  |    | |:|  :| ||| | ||     ||:  ::
Db        258 ---EDEKYLFSDDSSELTIRKVDKNDEAEYVCIAENKAG-----EQDASIH 300


RESULT 15
JC2457
vascular cell adhesion protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 08-Oct-1999
C;Accession: JC2457
R;Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
Biochem. Biophys. Res. Commun. 201, 805-812, 1 94
A;Title: Cloning and expression kinetics of po cine vascular cell adhesion molecule.
A;Reference number: JC2457; MUID:94271236; PMI :7516159
A;Accession: JC2457
A;Molecule type: mRNA
A;Residues: 1-538 <TSA>
A;Cross-references: EMBL:U08351; NID:g474382; IDN:AAA21542.1; PID:g474383
C;Keywords: glycoprotein; transmembrane protei:
F;497-517/Domain: transmembrane #status predic ed <TMM>
F;75,157,271,330,360/Binding site: carbohydrat (Asn) (covalent) #status predicted

  Query Match             9.8%;  Score 161;  D 2;  Length 538;
  Best Local Similarity   29.0%;  Pred. No. 1. e-05;
  Matches   58;  Conservative   23;  Mismatche   79;  Indels   40;  Gaps    8;

Qy         36 SSNRTPVVQEFESVELSCIITDSQTSDPRIEW: KIQDEQTTYVFFDNKIQGDLAGRAEIL 95
               | | :  :|| :|: ::|  |       |:| | |              ||  |  |:| |
Db        227 SVNPSTSLQEGDSMMMTC--TSEGLPAPQISW: K---------KLDNGDQQLLSGNA--- 272

Qy         96 GKTSLKIWNVTRRDSALYRCEVV--ARNDRKE: DEIVIELTVQVKP--VTPVCRVPKAVP 151
                  :| :  :   || :| || |     :|||     :||||| |   |          :
Db        273 ---TLTLIAMRMEDSGIYVCEGVNPVGTNRKE: ----VELTVQVAPRDTTISVNPSSTLE 324

Qy        152 VGKMATLHCQESEGHPRPHYSWYRNDVPLPTD: RANPRFRNSSFHLNSETGTLVFTAVHK 211
               |    : |  |:| | |   |              : : |: :    ||  ||  |:
Db        325 EGSSVNMTC-SSDGFPAPKILW-----------SKKLRDGNLEPLSENTTLTLTSTKM 370

Qy        212 DDSGQYYCIASNDAGSARCE 231
                :||| | |   | ||  | |
Db        371 EDSGIYVCEGINQAGINRKE 390


Search completed: June 15, 2004, 11:05:46
Job time : 15 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:51:49 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDPFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488	29.8	298	1	JAM2_HUMAN	P57087 homo sapien
2	457.5	27.9	300	1	JAM1_MOUSE	O88792 mus musculu
3	424	25.9	299	1	JAM1_HUMAN	Q9y624 homo sapien
4	408.5	25.0	298	1	JAM1_BOVIN	Q9xt56 bos taurus
5	228.5	14.0	319	1	A33_HUMAN	Q99795 homo sapien
6	186	11.4	1088	1	NCA1_XENLA	P16170 xenopus lae
7	177	10.8	1092	1	NCA2_XENLA	P36335 xenopus lae
8	174	10.6	333	1	AMAL_DROME	P15364 drosophila
9	171.5	10.5	725	1	NCA2_MOUSE	P13594 mus musculu
10	171.5	10.5	1115	1	NCA1_MOUSE	P13595 mus musculu
11	171	10.4	1377	1	NEO1_RAT	P97603 rattus norv
12	170	10.4	837	1	NCM2_HUMAN	O15394 homo sapien
13	169.5	10.4	858	1	NCA1_RAT	P13596 rattus norv
14	169.5	10.4	1912	1	PTPD_HUMAN	P23468 homo sapien
15	169	10.3	837	1	NCM2_MOUSE	O35136 mus musculu
16	164.5	10.0	3707	1	PGBM_MOUSE	Q05793 mus musculu
17	163.5	10.0	1051	1	PTK7_CHICK	Q91048 gallus gall
18	163	10.0	1091	1	NCA1_CHICK	P13590 gallus gall
19	163	10.0	1493	1	NEO1_MOUSE	P97798 mus musculu
20	161.5	9.9	853	1	NCA1_BOVIN	P31836 bos taurus
21	161	9.8	344	1	NTRI_HUMAN	Q9p121 homo sapien
22	160.5	9.8	761	1	NCA2_HUMAN	P13592 homo sapien
23	160.5	9.8	848	1	NCA1_HUMAN	P13591 homo sapien
24	159.5	9.7	365	1	CXAR_HUMAN	P78310 homo sapien
25	159.5	9.7	6632	1	UN89_CAEEL	O01761 caenorhabdi
26	159	9.7	353	1	CEPU_CHICK	Q90773 gallus gall
27	156	9.5	344	1	NTRI_MOUSE	Q99pj0 mus musculu
28	155.5	9.5	1284	1	NRCA_CHICK	P35331 gallus gall
29	155	9.5	344	1	NTRI_RAT	Q62718 rattus norv
30	153.5	9.4	1461	1	NEO1_HUMAN	Q92859 homo sapien
31	151.5	9.3	349	1	LACH_SCHAM	Q26474 schistocerc
32	150.5	9.2	702	1	CEA5_HUMAN	P06731 homo sapien
33	147.5	9.0	1897	1	PTPF_HUMAN	P10586 homo sapien
34	146.5	8.9	338	1	LAMP_RAT	Q62813 rattus norv
35	145.5	8.9	345	1	OPCM_RAT	P32736 rattus norv
36	145.5	8.9	4391	1	PGBM_HUMAN	P98160 homo sapien
37	145	8.9	338	1	LAMP_CHICK	Q98919 gallus gall
38	145	8.9	521	1	CEA1_MOUSE	P31809 mus musculu
39	144.5	8.8	338	1	LAMP_HUMAN	Q13449 homo sapien
40	144	8.8	847	1	CD22_HUMAN	P20273 homo sapien
41	143.5	8.8	1277	1	CAML_FUGRU	Q98902 fugu rubrip
42	143.5	8.8	1443	1	NEO1_CHICK	Q90610 gallus gall
43	142.5	8.7	646	1	MU18_HUMAN	P43121 homo sapien
44	142	8.7	365	1	CXAR_MOUSE	P97792 mus musculu
45	141	8.6	345	1	OPCM_BOVIN	P11834 bos taurus

ALIGNMENTS

RESULT 1
JAM2_HUMAN
ID JAM2_HUMAN STANDARD; PRT; 298 AA.
AC P57087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 2 precursor (Vascular endothelial
DE junction-associated molecule) (VE-JAM).
GN JAM2 OR VEJAM OR C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20507930; PubMed=10945976;
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J.,
RA Vanderslice P., Morris A.P., Brock T.A.;
RT "A novel protein with homology to the junctional adhesion molecule:
RT Characterization of leukocyte interactions.";
RL J. Biol. Chem. 275:34750-34756(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC       SECONDARY LYMPHOID ORGANS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC       VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC       LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC       CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3(2001);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF255910; AAF81223.1; -.
DR   EMBL; AY016009; AAG49022.1; -.
DR   EMBL; BC017779; AAH17779.1; -.
DR   Genew; HGNC:14686; JAM2.
DR   MIM; 606870; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    298       JUNCTIONAL ADHESION MOLECULE 2.
FT   DOMAIN       21    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    127       IG-LIKE V-TYPE.
FT   DOMAIN      134    238       IG-LIKE C2-TYPE.
FT   DISULFID     50    109       POTENTIAL.
FT   DISULFID    155    214       POTENTIAL.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    236    236       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  33207 MW;  CA78E518E22DCAEE CRC64;

  Query Match             29.8%;  Score 488;  DB 1;  Length 298;
  Best Local Similarity   36.2%;  Pred. No. 4.5e-33;
  Matches  115;  Conservative   60;  Mismatches  115;  Indels   28;  Gaps   10;

Qy          1 MALRRPPRLRLCARLPDPFPLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EPESVELSC 53
              || |   ||           |||| |  ::      |    :     ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |. | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  | ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVN 292
              : |:| |||| |||  |:||  |::: ||:| | |:||| :|:   |::   | :  :
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSS 280

Qy        293 YIRTDEEGDFRHKSSFVI 310

                  |  | ||:|  ||:|
Db        281 KATIMSENDFKHTKSFII 298


RESULT 2
JAM1_MOUSE
ID   JAM1_MOUSE     STANDARD;      PRT;   300 AA.
AC   O88792;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1 OR JCAM1 OR JCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98327120; PubMed=9660867;
RA   Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA   Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA   Simmons D., Dejana E.;
RT   "Junctional adhesion molecule, a novel member of the immunoglobulin
RT   superfamily that distributes at intercellular junctions and modulates
RT   monocyte transmigration.";
RL   J. Cell Biol. 142:117-127(1998).
RN   [2]
RP   INTERACTION WITH PARD3.
RX   MEDLINE=21340266; PubMed=11447115;
RA   Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA   Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
RT   "The cell polarity protein ASIP/PAR-3 directly associates with
RT   junctional adhesion molecule (JAM).";
RL   EMBO J. 20:3738-3748(2001).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX   MEDLINE=21391702; PubMed=11500366;
RA   Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA   Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA   Winkler F.K., Hennig M.;
RT   "X-ray structure of junctional adhesion molecule: structural basis for
RT   homophilic adhesion via a novel dimerization motif.";
RL   EMBO J. 20:4391-4398(2001).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly. Plays a role in regulating monocyte
CC       transmigration involved in integrity of epithelial barrier.
CC       Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC       Localized at tight junctions of both epithelial and endothelial
CC       cells.
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U89915; AAC32982.1; -.
DR   PDB; 1F97; 22-AUG-01.
DR   MGD; MGI:1321398; F11r.
```

```
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal; 3D-structure.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    300       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       27    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    122       IG-LIKE V-TYPE 1.
FT   DOMAIN      134    230       IG-LIKE V-TYPE 2.
FT   DISULFID     49    108       POTENTIAL.
FT   DISULFID    152    212       POTENTIAL.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32368 MW;  391F3B48FF3B97EC CRC64;

  Query Match             27.9%;  Score 457.5;  DB 1;  Length 300;
  Best Local Similarity   35.6%;  Pred. No. 1.5e-30;
  Matches  106;  Conservative   56;  Mismatches  121;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
              || ||   ::|::     :: ::     | | ||::|:|  | |  | ||:||| :|
Db         11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
              |  | ::::|    | |      : :   :|||:|:  | | :|:    :   |: | ||
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
              | | |  |   || :| :|  | | | | :| |   |||::: : : | |::    | ||
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
              || :: ::| |:|  |   |||:||| | |  |:| | |   |:  :||:|||:  |||
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              | :| |:  |:  || ||||   |:       |||    :   |  ||:|:  |||::
Db        247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 3
JAM1_HUMAN
ID   JAM1_HUMAN     STANDARD;      PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
DE   molecule 1) (PAM-1) (Platelet F11 receptor) (UNQ264/PRO301).
GN   F11R OR JAM1 OR JCAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA   Kornecki E.;
RT   "Molecular cloning and sequencing of the cDNA of F11 receptor, a
RT   novel Ig superfamily member from human platelets.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Naik U.P., Naik M.U., DeLeon P., Spychala J.;
RT   "Cloning and characterization of PAM-1, a novel platelet adhesion
RT   molecule involved in platelet activation.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
```

```
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111713; AAD42050.1; -.
DR   EMBL; AF207907; AAF22829.1; -.
DR   EMBL; AF172398; AAD48877.1; -.
DR   EMBL; AL136649; CAB66584.1; -.
DR   EMBL; AY358896; AAQ89255.1; -.
DR   EMBL; BC001533; AAH01533.1; -.
DR   PIR; A59406; S56749.
DR   Genew; HGNC:14685; F11R.
DR   MIM; 605721; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    299       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       26    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       27    125       IG-LIKE V-TYPE 1.
FT   DOMAIN      135    228       IG-LIKE V-TYPE 2.
FT   DISULFID     50    109       POTENTIAL.
FT   DISULFID    153    212       POTENTIAL.
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   299 AA;  32583 MW;  D95DE2FEA23D2851 CRC64;

  Query Match           25.9%;  Score 424;  DB 1;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.7e-28;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
                | |||: ||  || |||  :   |:|:| | | |  |:          ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                |||  | :| ::  ||  || ||:|   |:   |    |  |            ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 4
JAM1_BOVIN
ID   JAM1_BOVIN     STANDARD;      PRT;   298 AA.
AC   Q9XT56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111714; AAD42051.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    298       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       25    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    124       IG-LIKE V-TYPE 1.
FT   DOMAIN      134    227       IG-LIKE V-TYPE 2.
FT   DISULFID     49    108       POTENTIAL.
FT   DISULFID    152    211       POTENTIAL.
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  32456 MW;  714FE1C1714769A2 CRC64;

  Query Match           25.0%;  Score 408.5;  DB 1;  Length 298;
  Best Local Similarity   33.8%;  Pred. No. 1.6e-26;
  Matches  102;  Conservative   49;  Mismatches  124;  Indels   27;  Gaps   10;

Qy         21 LLLFRGCLI-------GAVNLKSSNRTPVVQ--EPESVELSCIITDSQTSDPRIEWKKIQ 71
              ||||   ::       |||          |||:  |    :|||  : |  | ||:|||
Db         12 LLLFTSMILCSLALGRGAV----QTYEPVVRVPENNPAKLSC--SYSGFSSPRVEWKFTH 65

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVI 131
              :    | ::|||       |      | :   :|||:|: :| | :|:        |: :
```

```
Db         66 GDIRGLVCYNNKITASYENRV-TFSDTGITFHSVTRKDTGMYTC-MVSDEGGNTYGEVTV 123

Qy        132 ELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFR 191
              :| | | |   || :| :|  | | | | :| |   | |::: | :| : ::|  |
Db        124 QLIVLVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEPKSNRAFS 183

Qy        192 NSSFHLNSETGTLVFTAVHKDDSGQYYCIASND-AGSARCEEQEMEVYDLNIGGIIGGVL 250
              |||: || :|| |:|  |   |:| : | | |  |   : :   |:  :||:|||:  |
Db        184 NSSYTLNQKTGELIFDPVSASDTGDFTCQAQNGYASPVKSDTVHMDAVELNVGGIVAAVF 243

Qy        251 VVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTD--EEGDFRHKSSF 308
              | | :|  :  ||  || ||||   |: | | |       | | : :   :|:||  |||
Db        244 VTLILLGALIFGIWFAYSRGYFDRAKK-GTSNKK------VIYSQPNARSDGEFRQTSSF 296

Qy        309 VI 310
              ::
Db        297 LV 298


RESULT 5
A33_HUMAN
ID   A33_HUMAN      STANDARD;      PRT;   319 AA.
AC   Q99795;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cell surface A33 antigen precursor (Glycoprotein A33).
GN   GPA33.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=97165045; PubMed=9012807;
RA   Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA   Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA   Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA   Burgess A.W.;
RT   "The human A33 antigen is a transmembrane glycoprotein and a novel
RT   member of the immunoglobulin superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN   [2]
RP   POST-TRANSLATIONAL MODIFICATIONS.
RX   MEDLINE=97396159; PubMed=9245713;
RA   Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA   Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA   Simpson R.J.;
RT   "Characterization of posttranslational modifications of human A33
RT   antigen, a novel palmitoylated surface glycoprotein of human
RT   gastrointestinal epithelium.";
RL   Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC   -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC       epithelium and in 95% of colon cancers.
CC   -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC       CARBOHYDRATE.
CC   -!- PTM: Palmitoylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U79725; AAC50957.1; -.
DR   Genew; HGNC:4445; GPA33.
DR   MIM; 602171; -.
DR   GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW   Transmembrane; Signal; Antigen.
FT   SIGNAL       1     21
FT   CHAIN       22    319       CELL SURFACE A33 ANTIGEN.
FT   DOMAIN      22    235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    236   256       POTENTIAL.
FT   DOMAIN      257   319       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      22    134       IG-LIKE V-TYPE.
FT   DOMAIN      140   227       IG-LIKE C2-TYPE.
FT   DOMAIN      258   261       POLY-CYS.
FT   DISULFID    43    117       POTENTIAL.
FT   DISULFID    146   222       POTENTIAL.
FT   DISULFID    162   211       POTENTIAL.
FT   CARBOHYD    112   112       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    200   200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223   223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   319 AA;  35632 MW;  9BFC7AAF45C2408E CRC64;

  Query Match             14.0%;  Score 228.5;  DB 1;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 1.3e-11;
  Matches   79;  Conservative   49;  Mismatches  128;  Indels   51;  Gaps   14;

Qy         29 IGAVNLKSSNRTPVVQEFESVELSCII-TDSQTSDPRIEWKKIQDEQTTYVF---FDNK- 83
              : |:::::       : :|| | |   | : : :  |:| |:    |  |    | ||
Db         19 VDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKN 78

Qy         84 -IQGDL-------AGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTV 135
               | |:|       :  ||     |: |  :|  |:  | | |   :| :   :  : | |
Db         79 YIHGELYKNRVSISNNAE-QSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLV 137

Qy        136 QVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDV-----PLPTDSRANPRF 190
              | |  | | :     :|    | ||  || | | ||| | ::     ||   :   |
Db        138 LVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQP-- 195

Qy        191 RNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE-EQEMEVYDLNIG---GII 246
                        :    : | || | | :||: |:  |     :    :|:    ||
Db        196 ------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIA 242

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFIN--NKQDG----ESYKNPGKPDGVNYI--RTDE 298
              ||:  | :: :|    ||   ||    |  :|:|     |:|: |  |: : :    :|
Db        243 VGVVAALIIIGIIIYCCCC---RGKDDNTEDKEDARPNREAYEEP--PEQLRELSREREE 297

Qy        299 EGDFRHK 305
              | |:| :
Db        298 EDDYRQE 304


RESULT 6
NCA1_XENLA
ID   NCA1_XENLA     STANDARD;      PRT;  1088 AA.
AC   P16170;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).
RX   MEDLINE=90098871; PubMed=2481269;
```

```
RA   Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT   "Primary structure and developmental expression of a large
RT   cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT   molecule (NCAM).";
RL   Nucleic Acids Res. 17:10321-10335(1989).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=N-CAM 180;
CC         IsoId=P16170-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P16170-2; Sequence=VSP_002589;
CC   -!- TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
CC       tissue.
CC   -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC       TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC       EARLY NEURAL DEVELOPMENT.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M25696; AAA49909.1; -.
DR   PIR; S09600; IJXLNL.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20   1088       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1088       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      209    294       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    484       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    804   1049       Missing (in isoform N-CAM 140).
FT                                /FTId=VSP_002589.
SQ   SEQUENCE   1088 AA;  117778 MW;  62738B55B03F3E83 CRC64;

  Query Match             11.4%;  Score 186;  DB 1;  Length 1088;
  Best Local Similarity   28.9%;  Pred. No. 1.8e-07;
  Matches   61;  Conservative   30;  Mismatches   84;  Indels   36;  Gaps   11;

Qy         30 GAVNLK-----SSNRTPVVQEPESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVPFDN 82
              | ||||     :    |  |||:  | : || |  :| |  | |: | :|      | |
Db        105 GTVNLKIYQKLTPKNAPTPQEPKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
               :      | :|    |:|  : : |    ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHL 197
              : :    ||     : :   | | :::| | |  || :   |:
Db        214 RQL----RVNATANMAESVVLSC-DADGPPDPEISWLKKGEPIEDG--------EEKISF 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :   | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 7
NCA2_XENLA
ID   NCA2_XENLA     STANDARD;      PRT;  1092 AA.
AC   P36335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93273239; PubMed=7684721;
RA   Tonissen K.F., Krieg P.A.;
RT   "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
RT   laevis are expressed during development and in adult tissues.";
RL   Gene 127:243-247(1993).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC         IsoId=P36335-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M76710; AAA49910.1; -.
DR   PIR; JN0635; JN0635.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
```

```
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 4.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19       BY SIMILARITY.
FT   CHAIN        20   1092       NEURAL CELL ADHESION MOLECULE 2, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1092       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    295       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    489       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1092 AA;  118082 MW;  CD236EE0EF8B7AD1 CRC64;

  Query Match           10.8%;  Score 177;  DB 1;  Length 1092;
  Best Local Similarity   28.6%;  Pred. No. 1e-06;
  Matches   60;  Conservative   28;  Mismatches   88;  Indels   34;  Gaps   10;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||   :       |  |||   | : || |  :| |  | |: | :|     | |
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
               :     | :|    |:|  : : |   ||||  ::||    ||:   |:: | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLN 198
              |||     : :   | | :::| | |  || :   |:                     |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDG--------EEKISFN 261
                                                                       ;

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
                :   :    | |:|  :| |||:| || |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 8
AMAL_DROME
ID   AMAL_DROME     STANDARD;      PRT;   333 AA.
AC   P15364; Q9V3A5;
DT   01-APR-1990 (Rel. 14, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amalgam protein precursor.
GN   AMA OR BG:DS00276.6 OR CG2198.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=89028670; PubMed=3141062;
RA   Seeger M.A., Haffley L., Kaufman T.C.;
RT   "Characterization of amalgam: a member of the immunoglobulin
RT   superfamily from Drosophila.";
RL   Cell 55:589-600(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA   Palazzolo M.J.;
RT   "Complete sequence of the Antennapedia complex of Drosophila.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
```

```
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------------
DR   EMBL; M23561; AAA28367.1; -.
DR   EMBL; AE001572; AAD19797.1; -.
DR   EMBL; AE003674; AAF54084.1; -.
DR   EMBL; AY051911; AAK93335.1; -.
DR   PIR; A31923; A31923.
DR   FlyBase; FBgn0000071; Ama.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
KW   Repeat.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24      ?       AMALGAM PROTEIN.
FT   PROPEP        ?    333       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       25    128       IG-LIKE V-TYPE.
FT   DOMAIN      139    223       IG-LIKE C2-TYPE 1.
FT   DOMAIN      230    323       IG-LIKE C2-TYPE 2.
FT   DISULFID     46    117       PROBABLE.
FT   DISULFID    161    208       PROBABLE.
FT   DISULFID    251    307       PROBABLE.
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     83     83       Q -> K (IN REF. 1).
SQ   SEQUENCE   333 AA;  36387 MW;  F644753DE3DB25F1 CRC64;

  Query Match             10.6%;  Score 174;  DB 1;  Length 333;
  Best Local Similarity   26.3%;  Pred. No. 4.2e-07;
  Matches   51;  Conservative   39;  Mismatches   84;  Indels   20;  Gaps    5;

Qy         35 KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEI 94
              ::: :: :| | :::||:|    :    | | | :            :    :     :
Db        143 ENTPKSTLVTEGQNLELTC--HANGFPKPTISWAR----------EHNAVMPAGGHL 187

Qy         95 LGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGK 154
              | : :|:| :| | |   | |  :|:|   : |: :| : |: :|   | |   | |
Db        188 LAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSH 245

Qy        155 MATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDS 214
              | | |   :|:| |   |::| |||   |  :    |::    : |  |    :| ::|
Db        246 SAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEEDF 302

Qy        215 GQYYCIASNDAGSA 228
              | ||| |:|  | |
Db        303 GDYYCNATNKLGHA 316


RESULT 9
NCA2_MOUSE
ID   NCA2_MOUSE     STANDARD;      PRT;   725 AA.
AC   P13594; Q61950;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE   (NCAM-120).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
RA   Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 20-700 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [3]
RP   SEQUENCE OF 642-725 FROM N.A.
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=Displayed;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=External;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ----------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------------
DR   EMBL; Y00051; CAA68263.1; -.
DR   EMBL; X15049; CAA33148.1; ALT_SEQ.
DR   EMBL; X07195; CAA30173.1; -.
DR   PIR; A29673; IJMSNG.
DR   PDB; 2NCM; 12-MAR-97.
DR   PDB; 3NCM; 23-JUL-99.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
KW   Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
KW   3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    725       NEURAL CELL ADHESION MOLECULE 1, 120 kDa
FT                                 ISOFORM.
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
```

```
FT   DOMAIN       212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN       309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN       407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN       519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN       625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN       152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN       161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID      41     96       PROBABLE.
FT   DISULFID     139    189       PROBABLE.
FT   DISULFID     235    288       PROBABLE.
FT   DISULFID     330    386       PROBABLE.
FT   DISULFID     427    480       PROBABLE.
FT   CARBOHYD     222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     261    268       ERSRSSVS -> DEKHIFSD (IN REF. 2).
FT   CONFLICT     273    273       V -> L (IN REF. 2).
FT   CONFLICT     354    355       QD -> KT (IN REF. 2).
FT   CONFLICT     549    549       T -> K (IN REF. 2).
FT   CONFLICT     572    572       T -> R (IN REF. 2).
FT   CONFLICT     575    575       D -> V (IN REF. 2).
FT   CONFLICT     589    594       MQPSES -> SAATEF (IN REF. 2).
FT   CONFLICT     600    602       PEL -> REP (IN REF. 2).
FT   CONFLICT     657    657       H -> D (IN REF. 2 AND 3).
SQ   SEQUENCE   725 AA;  80296 MW;  C2AEB8B4461C6B2F CRC64;

  Query Match           10.5%;  Score 171.5;  DB 1;  Length 725;
  Best Local Similarity  27.3%;  Pred. No. 1.8e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |         ||:|   :       | |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  |  :|    |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |:: | | |      :  |     :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
               | |:|     |::  :    | |:|  :| ||| | ||     ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 10
NCA1_MOUSE
ID   NCA1_MOUSE     STANDARD;      PRT;  1115 AA.
AC   P13595; Q61949;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
DE   (NCAM-180).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
RA   Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6;
RX   MEDLINE=88067687; PubMed=3684567;
RA   Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,
RA   Goridis C., Wille W.;
RT   "Analysis of cDNA clones that code for the transmembrane forms of the
RT   mouse neural cell adhesion molecule (NCAM) and are generated by
RT   alternative RNA splicing.";
RL   Nucleic Acids Res. 15:8621-8641(1987).
RN   [3]
RP   SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=88247737; PubMed=2454455;
RA   Barthels D., Vopper G., Wille W.;
RT   "NCAM-180, the large isoform of the neural cell adhesion molecule of
RT   the mouse, is encoded by an alternatively spliced transcript.";
RL   Nucleic Acids Res. 16:4217-4225(1988).
RN   [5]
RP   SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [6]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=VSP_002588;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07200; CAA30177.1; -.
DR   EMBL; Y00051; -; NOT_ANNOTATED_CDS.
DR   EMBL; X06328; CAA29641.1; -.
DR   EMBL; X07195; CAA30173.1; -.
DR   EMBL; X07244; CAA30230.1; -.
DR   EMBL; X15051; CAA33150.1; -.
DR   EMBL; X15052; CAA33151.1; -.
DR   PIR; A29673; IJMSNL.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
```

```
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
FT   SIGNAL        1     19
FT   CHAIN        20   1115       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                               ISOFORM.
FT   DOMAIN       20    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    729       POTENTIAL.
FT   DOMAIN      730   1115       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
FT   DISULFID    139    189       PROBABLE.
FT   DISULFID    235    288       PROBABLE.
FT   DISULFID    330    386       PROBABLE.
FT   DISULFID    427    480       PROBABLE.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    810   1076       Missing (in isoform N-CAM 140).
FT                               /FTId=VSP_002588.
SQ   SEQUENCE   1115 AA;  119351 MW;  2C93DCD474CFBCAF CRC64;

  Query Match             10.5%;  Score 171.5;  DB 1;  Length 1115;
  Best Local Similarity   27.3%;  Pred. No. 3e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |         ||:|  :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   | :: |:  |  :|     |:|  : : |    ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RPIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |:: | | |     :  |     :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
               | |:|     |::  :    | |:|  :| ||| | ||     ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 11
NEO1_RAT
ID   NEO1_RAT       STANDARD;      PRT;  1377 AA.
AC   P97603;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neogenin precursor (Fragment).
GN   NEO1 OR NGN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97015074; PubMed=8861902;
RA   Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.-Y.,
RA   Culotti J.G., Tessier-Lavigne M.;
RT   "Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
RL   Cell 87:175-185(1996).
CC   -!- FUNCTION: May be involved as a regulatory protein in the
CC       transition of undifferentiated proliferating cells to their
CC       differentiated state. May also function as a cell adhesion
CC       molecule in a broad spectrum of embryonic and adult tissues.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. DCC family.
CC   -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U68726; AAB41100.1; -.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 6.
DR   Pfam; PF00047; ig; 4.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 6.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW   Glycoprotein.
FT   NON_TER       1      1
FT   SIGNAL       <1      2       POTENTIAL.
FT   CHAIN         3   1377       NEOGENIN.
FT   DOMAIN        3   1074       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1075   1095       POTENTIAL.
FT   DOMAIN     1096   1377       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21    114       IG-LIKE C2-TYPE 1.
FT   DOMAIN      121    206       IG-LIKE C2-TYPE 2.
FT   DOMAIN      198    305       IG-LIKE C2-TYPE 3.
FT   DOMAIN      310    395       IG-LIKE C2-TYPE 4.
FT   DOMAIN      405    502       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      505    598       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      599    698       FIBRONECTIN TYPE-III 3.
FT   DOMAIN      704    798       FIBRONECTIN TYPE-III 4.
FT   DOMAIN      819    919       FIBRONECTIN TYPE-III 5.
FT   DOMAIN      920   1021       FIBRONECTIN TYPE-III 6.
FT   DOMAIN     1087   1090       POLY-VAL.
FT   DISULFID     43     98       BY SIMILARITY.
FT   DISULFID    142    190       BY SIMILARITY.
FT   DISULFID    239    289       BY SIMILARITY.
FT   DISULFID    331    379       BY SIMILARITY.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    439    439       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    458    458       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    608    608       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    684    684       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    878    878       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1377 AA;  150637 MW;  E514ED8ABD1A63A9 CRC64;

  Query Match             10.4%;  Score 171;  DB 1;  Length 1377;
```

```
  Best Local Similarity   31.5%;  Pred. No. 4.2e-06;
  Matches   62;  Conservative   20;  Mismatches   69;  Indels   46;  Gaps    9;

Qy          47 ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVT 106
               :|  | |:   |    | | | | :|   |          : :||  :|   ||:| :||
Db         233 QSAVLPCVA--SGLPAPVIRWMKNEDVLDT----------ESSGRLALLAGGSLEISDVT 280

Qy         107 RRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQES--- 163
                 |:  | |  || |  | | |   ||||||  |            : : | :: :||
Db         281 EDDAGTYFC--VADNGNKTI-EAQAELTVQVPPEF----------LKQPANIYARESMDI 327

Qy         164 ------EGHPRPHYSWYRN-DVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQ 216
                   | | |   | :| || :|:|          | :  |    |   | | | ||
Db         328 VFECEVTGKPAPTVKWVKNGDVVIPSD----------YFKIVKEHNLQVLGLV-KSDEGF 376

Qy         217 YYCIASNDAGSARCEEQ 233
               | ||| || |:|:   |
Db         377 YQCIAENDVGNAQAGAQ 393


RESULT 12
NCM2_HUMAN
ID   NCM2_HUMAN     STANDARD;      PRT;   837 AA.
AC   O15394;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN   NCAM2 OR NCAM21.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97369930; PubMed=9226371;
RA   Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
RT   "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
RT   that maps to chromosome region 21q21 and is potentially involved in
RT   Down syndrome.";
RL   Genomics 43:43-51(1997).
RN   [2]
RP   CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX   MEDLINE=22660472; PubMed=12754519;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
CC   -!- FUNCTION: May play important roles in selective fasciculation and
CC       zone-to-zone projection of the primary olfactory axons.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC       brain.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U75330; AAB80803.1; -.
DR   Genew; HGNC:7657; NCAM2.
DR   MIM; 602040; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    837       NEURAL CELL ADHESION MOLECULE 2.
FT   DOMAIN       20    697       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    698    718       POTENTIAL.
FT   DOMAIN      719    837       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    297       IG-LIKE C2-TYPE 3.
FT   DOMAIN      302    396       IG-LIKE C2-TYPE 4.
FT   DOMAIN      401    491       IG-LIKE C2-TYPE 5.
FT   DOMAIN      482    581       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      594    678       FIBRONECTIN TYPE-III 2.
FT   DISULFID     42     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    281       PROBABLE.
FT   DISULFID    322    380       PROBABLE.
FT   DISULFID    422    475       PROBABLE.
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    309    309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    419    419       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    445    445       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    474    474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    562    562       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   837 AA;  92932 MW;  C3D034106C5741C1 CRC64;

  Query Match             10.4%;  Score 170;  DB 1;  Length 837;
  Best Local Similarity   24.3%;  Pred. No. 2.8e-06;
  Matches   72;  Conservative   32;  Mismatches  104;  Indels   88;  Gaps   15;

Qy          44 QEF---ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSL 100
               |||   |  |: | :: |    | : |    :| ||    ||         | :| :|
Db         124 QEFKQGEDAEVVCRVSSSPA--PAVSWLYHNEEVTT--ISDN--------RLAMLANNNL 171

Qy         101 KIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV------ 152
               :| |: : |  :|||  | || :            :  : : :  || |: :
Db         172 QILNINKSDEGIYRCEGRVEARGE-----------IDFRDIIVIVNVPPAISMPQKSFN 219

Qy         153 -----GKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFT 207
                    |:  |  |: | | | |  ||:||   :          |  : |      |
Db         220 ATAERGEEMTFSCRAS-GSPEPAISWFRNGKLIE---------ENEKYILKGSNTELTVR 269

Qy         208 AVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAY 267
                :  | | | | |:| ||    | | : :           | |     :| |     |
Db         270 NIINSDGGPYVCRATNKAG-----EDEKQAP----------LQVFVQPHIIQLKNETTY 313

Qy         268 RRGYFINNKQDGESYKNPGKP----------DGVNYIRTDEEGDFR------HKSS 307
                 |  :    | |      |:|          ||  :   |:  | |      | ||
Db         314 ENGQ-VTLVCDAE-----GEPIPEITWKRAVDGFTFTEGDKSPDGRIEVKGQHGSS 363


RESULT 13
NCA1_RAT
ID   NCA1_RAT       STANDARD;      PRT;   858 AA.
AC   P13596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE   (NCAM-140).
GN   NCAM1 OR NCAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88059265; PubMed=3680385;
RA   Small S.J., Shull G.E., Santoni M.-J., Akeson R.;
RT   "Identification of a cDNA clone that contains the complete coding
RT   sequence for a 140-kD rat NCAM polypeptide.";
RL   J. Cell Biol. 105:2335-2345(1987).
RN   [2]
RP   SEQUENCE OF 355-364 FROM N.A.
RX   MEDLINE=90166485; PubMed=2483093;
RA   Small S.J., Haines S.L., Akeson R.A.;
RT   "Polypeptide variation in an N-CAM extracellular immunoglobulin-like
RT   fold is developmentally regulated through alternative splicing.";
RL   Neuron 1:1007-1017(1988).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC         IsoId=P13596-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X06564; CAA29809.1; -.
DR   EMBL; M32611; AAA41679.1; -.
DR   PIR; S00846; IJRTNC.
DR   PDB; 1EPP; 27-OCT-00.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
KW   3D-structure.
FT   SIGNAL       1     19
FT   CHAIN       20    858       NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT                               ISOFORM.
FT   DOMAIN       20    721       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    722    739       POTENTIAL.
FT   DOMAIN      740    858       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    414       IG-LIKE C2-TYPE 4.
FT   DOMAIN      417    502       IG-LIKE C2-TYPE 5.
FT   DOMAIN      514    615       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      616    712       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       BY SIMILARITY.
FT   DISULFID    139    189       BY SIMILARITY.
FT   DISULFID    235    288       BY SIMILARITY.
FT   DISULFID    330    396       BY SIMILARITY.
FT   DISULFID    437    490       BY SIMILARITY.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    460    460       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   858 AA;  94658 MW;  BA1A06A4EA0550F6 CRC64;

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 858;
  Best Local Similarity   26.3%;  Pred. No. 3.2e-06;
  Matches   61;  Conservative   42;  Mismatches   84;  Indels   45;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEPESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|    :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  | :|     |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |:: | | |      :  |     :|:  || | :::| | |  || ::  |:  :  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEEDD 261

Qy        188 PRFRNSSFHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
               :      |: : ::  |    | |:|  :| ||| | ||     ||:  ::
Db        262 EK------HIFSDDSSELTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 14
PTPD_HUMAN
ID   PTPD_HUMAN     STANDARD;      PRT;  1912 AA.
AC   P23468;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
DE   delta).
GN   PTPRD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX   MEDLINE=95204468; PubMed=7896816;
RA   Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT   "Molecular characterization of the human transmembrane protein-
RT   tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT   alternative human transmembrane protein-tyrosine phosphatase delta
RT   isoforms.";
RL   J. Biol. Chem. 270:6722-6728(1995).
RN   [2]
RP   SEQUENCE OF 390-1912 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91006018; PubMed=2170109;
RA   Krueger N.X., Streuli M., Saito H.;
RT   "Structural diversity and evolution of human receptor-like protein
RT   tyrosine phosphatases.";
RL   EMBO J. 9:3241-3252(1990).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P23468-1; Sequence=Displayed;
CC       Name=2; Synonyms=Kidney;
CC         IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC       Name=3; Synonyms=Fetal brain;
CC         IsoId=P23468-3; Sequence=VSP_005150;
CC   -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
```

```
CC       FROM THE TRANSMEMBRANE SEGMENT.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC   -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L38929; AAC41749.1; -.
DR   EMBL; X54133; CAA38068.1; -.
DR   PIR; A56178; A56178.
DR   HSSP; P18052; 1YFO.
DR   Genew; HGNC:9668; PTPRD.
DR   MIM; 601598; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR   GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 8.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00102; Y_phosphatase; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 8.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21   1912       PROTEIN-TYROSINE PHOSPHATASE DELTA.
FT   DOMAIN       21   1265       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1266   1290       POTENTIAL.
FT   DOMAIN     1291   1912       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       24    114       IG-LIKE C2-TYPE 1.
FT   DOMAIN      126    224       IG-LIKE C2-TYPE 2.
FT   DOMAIN      236    318       IG-LIKE C2-TYPE 3.
FT   DOMAIN      320    414       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      417    513       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      516    606       FIBRONECTIN TYPE-III 3.
FT   DOMAIN      609    708       FIBRONECTIN TYPE-III 4.
FT   DOMAIN      711    822       FIBRONECTIN TYPE-III 5.
FT   DOMAIN      825    916       FIBRONECTIN TYPE-III 6.
FT   DOMAIN      918   1017       FIBRONECTIN TYPE-III 7.
FT   DOMAIN     1020   1137       FIBRONECTIN TYPE-III 8.
FT   DOMAIN     1375   1618       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN     1619   1912       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   ACT_SITE   1553   1553       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   ACT_SITE   1844   1844       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   SITE       1175   1178       CLEAVAGE (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    299    299       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    724    724       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    832    832       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    181    189       Missing (in isoform 2).
FT                                /FTId=VSP_005147.
FT   VARSPLIC    226    229       Missing (in isoform 2).
FT                                /FTId=VSP_005148.
FT   VARSPLIC    775    783       Missing (in isoform 2).
FT                                /FTId=VSP_005149.
FT   VARSPLIC    609   1137       Missing (in isoform 3).
FT                                /FTId=VSP_005150.
FT   MUTAGEN    1178   1178       R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
SQ   SEQUENCE   1912 AA;  214759 MW;  3AE8CBCD32182E26 CRC64;

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 1912;
  Best Local Similarity   28.6%;  Pred. No. 8.5e-06;
  Matches   65;  Conservative   35;  Mismatches   76;  Indels   51;  Gaps   13;

Qy         39 RTPVVQEFESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRA 92
              |||| |    |  ::  |  : | |||  | |     ||: :::   : ||:       |
Db         28 RTPVDQTGVSGGVASFICQA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSG 79

Qy         93 EILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV 152
                :|    |:    | || |:| |  || |:  ||  :   |||  :      ::|:  |
Db         80 SVLRIQPLR----TPRDEAIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGPPT 127

Qy        153 GKM------------ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSE 200
                |            ||: |  | |:| |  :|::: :|: | |  | | :     | ||
Db        128 IDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSE 181

Qy        201 T-------GTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
                :       | |      : | |:| |:|:| ||:       : | :|
Db        182 SIGGTPIRGALQIEQSEESDQGKYECVATNSAGTRYSAPANLYVREL 228


RESULT 15
NCM2_MOUSE
ID   NCM2_MOUSE     STANDARD;      PRT;   837 AA.
AC   O35136; O35962;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE   adhesion molecule) (R4B12).
GN   NCAM2 OR OCAM OR RNCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC   STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX   MEDLINE=97368238; PubMed=9221781;
RA   Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA   Kagamiyama H., Mori K.;
RT   "OCAM: A new member of the neural cell adhesion molecule family
RT   related to zone-to-zone projection of olfactory and vomeronasal
RT   axons.";
RL   J. Neurosci. 17:5830-5842(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX   MEDLINE=97476194; PubMed=9334170;
RA   Alenius M., Bohm S.;
RT   "Identification of a novel neural cell adhesion molecule-related gene
RT   with a potential role in selective axonal projection.";
RL   J. Biol. Chem. 272:26083-26086(1997).
CC   -!- FUNCTION: May play important roles in selective fasciculation and
CC       zone-to-zone projection of the primary olfactory axons.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC       attached to the membrane by a GPI-anchor (short isoform).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=O35136-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=O35136-2; Sequence=VSP_002590;
CC   -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
```

```
CC       vomeronasal neurons in a zone-specific manner.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF001287; AAB69125.1; -.
DR   EMBL; AF001286; AAB69124.1; -.
DR   EMBL; AF016619; AAC53375.1; -.
DR   MGD; MGI:97282; Ncam2.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW   Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    837       NEURAL CELL ADHESION MOLECULE 2.
FT   DOMAIN       20    697       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    698    718       POTENTIAL.
FT   DOMAIN      719    837       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    297       IG-LIKE C2-TYPE 3.
FT   DOMAIN      302    396       IG-LIKE C2-TYPE 4.
FT   DOMAIN      401    491       IG-LIKE C2-TYPE 5.
FT   DOMAIN      482    581       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      594    678       FIBRONECTIN TYPE-III 2.
FT   DISULFID     42     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    281       PROBABLE.
FT   DISULFID    322    380       PROBABLE.
FT   DISULFID    422    475       PROBABLE.
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    309    309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    419    419       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    445    445       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    474    474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    562    562       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    694    837       TLFNGLGLGAIIGLGVAALLLILVVTDVSCFFIRQCGLLMC
FT                                ITRRMCGKKSGSSGKSKELEEGKAAYLKDGSKEPIVEMRTE
FT                                DERITNHEDGSPVNEPNETTPLTEPEKLPLKEENGKEVLNA
FT                                ETIEIKVSNDIIQSKEDDIKA -> NCCEANKGENGGQSWH
FT                                LNAVGFTFVITMSLSCLF (in isoform Short).
FT                                /FTId=VSP_002590.
SQ   SEQUENCE   837 AA;  93203 MW;  70473B053A2D65A5 CRC64;

  Query Match             10.3%;  Score 169;  DB 1;  Length 837;
  Best Local Similarity   29.3%;  Pred. No. 3.4e-06;
  Matches   58;  Conservative   25;  Mismatches   79;  Indels   36;  Gaps   10;

Qy         44 QEP---ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSL 100
              |||    |  |: | :: |    | : |    :| ||    ||        |  :|   :|
Db        124 QEFKQGEDAEVVCRVSSSPA--PAVSWLYHNEEVTTIP--DN--------RFAVLANNNL 171

Qy        101 KIWNVTRRDSALYRCE--VVARNDRKEID--EIVIELTVQVKPVTPVCRVPKAVPVGKMA 156
              :| |: : |  :|||| | ||    |||  :|:: : |    : |          |:
Db        172 QILNINKSDEGIYRCEGRVEARG---EIDFRDIIVIVNVPPAIMMPQKSFNATAERGEEM 228

Qy        157 TLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQ 216
              || |: | | | |  ||:||   :          |  : |      |    :  | |
Db        229 TLTCKAS-GSPDPTISWFRNGKLIE---------ENEKYILKGSNTELTVRNIINKDGGS 278

Qy        217 YYCIASNDAGSARCEEQE 234
              | | |:| ||    |:|:
Db        279 YVCKATNKAG----EDQK 292


Search completed: June 15, 2004, 11:03:40
Job time : 11 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:58:19 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1637	100.0	310	4	Q9BX67	Q9bx67 homo sapien
2	1637	100.0	355	4	Q8WWL8	Q8wwl8 homo sapien
3	1628	99.5	309	4	Q96FL1	Q96fl1 homo sapien
4	1425	87.0	310	11	Q9D8B7	Q9d8b7 mus musculu
5	1423	86.9	310	11	Q9EPK4	Q9epk4 mus musculu
6	1411	86.2	310	11	Q9D1M9	Q9d1m9 mus musculu
7	486.5	29.7	298	11	Q9JI59	Q9ji59 mus musculu
8	486.5	29.7	298	11	Q8C5K9	Q8c5k9 mus musculu
9	483.5	29.5	298	11	Q8CE95	Q8ce95 mus musculu
10	463.5	28.3	300	11	Q9JHY1	Q9jhy1 rattus norv
11	460	28.1	289	13	Q7ZWT0	Q7zwt0 xenopus lae
12	457.5	27.9	300	11	Q8VC39	Q8vc39 mus musculu
13	440.5	26.9	300	13	Q7SYQ7	Q7syq7 xenopus lae
14	336	20.5	259	4	Q9Y5B2	Q9y5b2 homo sapien
15	326	19.9	173	11	Q9JKD5	Q9jkd5 rattus norv
16	291	17.8	64	11	Q8BT59	Q8bt59 mus musculu
17	243.5	14.9	304	11	Q9CVA4	Q9cva4 mus musculu
18	242	14.8	318	13	Q91664	Q91664 xenopus lae
19	242	14.8	327	4	Q96IQ7	Q96iq7 homo sapien
20	240.5	14.7	284	4	Q9NX42	Q9nx42 homo sapien
21	240.5	14.7	325	4	O95791	O95791 homo sapien
22	233.5	14.3	328	11	Q9Z109	Q9z109 mus musculu
23	221.5	13.5	319	11	Q922D5	Q922d5 mus musculu
24	216	13.2	407	11	Q9D2J4	Q9d2j4 mus musculu
25	215.5	13.2	319	11	Q9JKA5	Q9jka5 mus musculu
26	206.5	12.6	248	11	Q9D0T4	Q9d0t4 mus musculu
27	206.5	12.6	335	13	Q9PWR4	Q9pwr4 gallus gall
28	203.5	12.4	335	13	Q9YGH1	Q9ygh1 gallus gall
29	203	12.4	181	13	Q91665	Q91665 xenopus lae
30	199.5	12.2	372	13	Q90Y50	Q90y50 brachydanio
31	198.5	12.1	335	13	Q9YGV5	Q9ygv5 gallus gall
32	197.5	12.1	387	4	Q86XK7	Q86xk7 homo sapien
33	193.5	11.8	373	4	Q9H6B4	Q9h6b4 homo sapien
34	193.5	11.8	795	13	Q90YM0	Q90ym0 brachydanio
35	189.5	11.6	358	13	Q90490	Q90490 brachydanio
36	188.5	11.5	1409	13	Q8JI27	Q8ji27 brachydanio
37	188.5	11.5	1409	13	Q801M2	Q801m2 brachydanio
38	188.5	11.5	1428	13	Q8AY67	Q8ay67 brachydanio
39	188	11.5	259	4	Q7Z2Q1	Q7z2q1 homo sapien
40	187.5	11.5	838	13	Q90YM1	Q90ym1 brachydanio
41	187	11.4	725	13	O73633	O73633 xenopus lae
42	182.5	11.1	372	11	Q8K1G0	Q8k1g0 rattus norv
43	180.5	11.0	300	11	Q9DA22	Q9da22 mus musculu
44	180.5	11.0	300	11	Q9D9J0	Q9d9j0 mus musculu
45	180.5	11.0	1894	11	Q64487	Q64487 mus musculu

ALIGNMENTS

RESULT 1
Q9BX67
ID Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion
DE molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesional Molecule-3 on Human
RT Platelets: A New Member of Immunoglobulin Superfamily.";

```
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   EMBL; AF448478; AAM20925.1; -.
DR   EMBL; AK074769; BAC11195.1; -.
DR   EMBL; AK075309; BAC11538.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;

  Query Match             100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-153;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
Q8WWL8
ID   Q8WWL8      PRELIMINARY;      PRT;   355 AA.
AC   Q8WWL8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule 3.
GN   JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hearn T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Phillips H.M.;
RT   "Narrowing the critical region within 11q24-qter for hypoplastic left
RT   heart and identification of a candidate gene, JAM3, expressed during
RT   cardiogenesis.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416101; CAC94776.1; -.
DR   Genew; HGNC:15532; JAM3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   CHAIN       76    355       JUNCTION ADHESION MOLECULE 3.
SQ   SEQUENCE   355 AA;  39602 MW;  8B1577DEA7B1D4F8 CRC64;

  Query Match             100.0%;  Score 1637;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-153;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 105

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 165

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 225

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 285

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 345

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        346 DFRHKSSFVI 355


RESULT 3
Q96FL1
ID   Q96FL1      PRELIMINARY;      PRT;   309 AA.
AC   Q96FL1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010690; AAH10690.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
FT   NON_TER      1      1
SQ   SEQUENCE   309 AA;  34917 MW;  50C5B1B7872E8DF3 CRC64;

  Query Match             99.5%;  Score 1628;  DB 4;  Length 309;
  Best Local Similarity   99.7%;  Pred. No. 3e-152;
  Matches  308;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          2 ALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTS 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTS 60

Qy         62 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 120

Qy        122 DRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 181
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 180

Qy        182 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240

Qy        242 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 300

Qy        302 FRHKSSFVI 310
              |||||||||
Db        301 FRHKSSFVI 309
```

RESULT 4
Q9D8B7
ID Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 87.0%; Score 1425; DB 11; Length 310;
Best Local Similarity 86.5%; Pred. No. 3.4e-132;

Matches 268; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||:| |||||||| ||||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPDFPLLLLFRGCMIEAVNLKSSNRNPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:|||||||||||| :: ||||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||||:|||||:||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYNWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   EMBL; BC024357; AAH24357.1; -.
DR   EMBL; AK032833; BAC28049.1; -.
DR   MGD; MGI:1933825; Jam3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;

  Query Match             86.9%;  Score 1423;  DB 11;  Length 310;
  Best Local Similarity   86.5%;  Pred. No. 5.4e-132;
  Matches  268;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||||:| |||||||| ||| ||||||||||||||||
Db          1 MALSRRLRLRLYARLPDPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
Q9D1M9
ID   Q9D1M9      PRELIMINARY;      PRT;   310 AA.
AC   Q9D1M9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003326; BAB22715.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34819 MW;  6692BCAD68EA4B1D CRC64;

  Query Match             86.2%;  Score 1411;  DB 11;  Length 310;
  Best Local Similarity   85.5%;  Pred. No. 8.2e-131;
  Matches  265;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||||:| |||||||| ||| ||||||||||||||||
Db          1 MALSRRLRLRLYARLPDPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||:|| :|||
Db        301 DFKHKIAFVI 310


RESULT 7
Q9JI59
ID   Q9JI59      PRELIMINARY;      PRT;   298 AA.
AC   Q9JI59;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial junction-associated molecule (Junctional adhesion
DE   molecule-3) (2410030G21Rik protein).
GN   JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20317114; PubMed=10779521;
RA   Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT   "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT   the Immunoglobulin Superfamily, Is Localized to Intercellular
RT   Boundaries of Endothelial Cells.";
RL   J. Biol. Chem. 275:19139-19145(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=11036763;
RA   Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT   Family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF255911; AAF81224.1; -.
DR   EMBL; AJ291757; CAC20699.1; -.
DR   EMBL; AK013914; BAB29053.1; -.
DR   EMBL; AK010616; BAB27064.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33047 MW;  1124E0F07E6CF751 CRC64;

  Query Match             29.7%;  Score 486.5;  DB 11;  Length 298;
  Best Local Similarity   36.7%;  Pred. No. 1.7e-39;
  Matches  114;  Conservative   54;  Mismatches  116;  Indels   27;  Gaps    9;

Qy         13 ARLPDPFFLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
              || |   |:||    || |::   :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGPSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
              |:||||:  :  : |::   :|||   |||::   :::| |||| |:  ||||| |  ::
Db         61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
               : : |  : | | | |  | || :|  | :  | ||: ||:| | | |:::     |
Db        119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy        183 DSRANPR---FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                 ||:     |||: :|:::| | |  : | |||:||| | |  |  ||  : |:|
Db        175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
              ||| |||  |:||  |:::  || | | |:|||        |:   | |   : : | |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
              ||:|  ||:|
Db        288 NDFKHTKSFII 298


RESULT 8
Q8C5K9
ID   Q8C5K9      PRELIMINARY;      PRT;   298 AA.
AC   Q8C5K9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK078128; BAC37139.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33182 MW;  1131F0BFD89CEB51 CRC64;

  Query Match             29.7%;  Score 486.5;  DB 11;  Length 298;
  Best Local Similarity   37.0%;  Pred. No. 1.7e-39;
  Matches  115;  Conservative   54;  Mismatches  115;  Indels   27;  Gaps    9;

Qy         13 ARLPDPFFLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
              || |   |:||    || |::   :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGPSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
              |:||||:  :  : |::   :|||   |||::   :::| |||| |:  ||||| |  ::
Db         61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
               : : |  : | | | |  | || :|  | :  | ||: ||:| | | |:::     |
Db        119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDGHSL-- 176

Qy        183 DSRANPRFR---NSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                 ||: |   |||: :|:::| | |  : | |||:||| | |  |  ||  : |:|
Db        177 --LGNPKGRTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
              ||| |||  |:||  |:::  || | | |:|||        |:   | |   : : | |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
              ||:|  ||:|
Db        288 NDFKHTKSFII 298


RESULT 9
Q8CE95
ID   Q8CE95      PRELIMINARY;      PRT;   298 AA.
AC   Q8CE95;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
```

```
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK028757; BAC26102.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33079 MW;  CB8227EC13D349A3 CRC64;

  Query Match             29.5%;  Score 483.5;  DB 11;  Length 298;
  Best Local Similarity   36.3%;  Pred. No. 3.5e-39;
  Matches  113;  Conservative   55;  Mismatches  116;  Indels   27;  Gaps    9;

Qy          13 ARLPDFFLLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
               || |    |:||     || |::   :|          :   | ||:    |:|  |  :|:
Db           2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEPQEAILAC-KTPKKTTSS 60

Qy          64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
               |:||||:   :  : |::   :|||   |||::   :::| |||| |:  |||||  |  ::
Db          61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy         124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
                : : |  : | | : |  | | || :|  | :  | ||: ||:| | | |:::     |
Db         119 GQNLQEDKVMLEVLMAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy         183 DSRANPR---FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                  ||:     |||: :|:::| | |   : | |||:||| | |   |   ||  : |:|
Db         175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy         240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
               ||| |||   |:||  |:::  || | | |:|||        |:    | |   : : |  |
Db         235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy         300 GDFRHKSSFVI 310
                ||:|  ||:|
Db         288 NDFKHTKSFII 298


RESULT 10
Q9JHY1
ID   Q9JHY1      PRELIMINARY;      PRT;   300 AA.
AC   Q9JHY1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule JAM.
GN   JAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley;
RA   Mashima H., Kojima I.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF276998; AAF78250.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   300 AA;  32369 MW;  45AE362A96158BFA CRC64;

  Query Match             28.3%;  Score 463.5;  DB 11;  Length 300;
  Best Local Similarity   37.9%;  Pred. No. 3.3e-37;
  Matches  113;  Conservative   49;  Mismatches  121;  Indels   15;  Gaps    8;

Qy          20 LLLLFRGCLIGA-VNLKSSNRTP----VVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
               || ||    ::|: |  | |  :|      | | :||:| ||    |  | ||:||| :|
Db          11 LLFLFTSMILGSLVQGKGSVYSPQTAVQVPENDSVKLPCIY--SGFSSPRVEWKFVQGST 68

Qy          75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
               |  | ::|:|     | |       : :   :|||:|:   | | :|: : :   |: | ||
Db          69 TALVCYNNQITVPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEDGGQNYGEVSIHLT 126

Qy         135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRPRNS 193
               | | |   :| :| :|  | | | | :| |   |||::: ||: | |::     | ||
Db         127 VLVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAPINS 186

Qy         194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
               |: :: ::| |||   |   |||:||| | |  |:| | |   ||  :||:|||:  |||
Db         187 SYTIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVT 246

Qy         253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               | :| |:  ||  || |||||   |:        |||    :       ||:|:  |||::
Db         247 LILLGLLIFGIWFAYSRGYFERTKKG----TAPGKKVIYSQPSARSEGEFKQTSSFLV 300


RESULT 11
Q7ZWT0
ID   Q7ZWT0      PRELIMINARY;      PRT;   289 AA.
AC   Q7ZWT0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to junctional adhesion molecule 1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046720; AAH46720.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   289 AA;  31630 MW;  24354B5A37618845 CRC64;

  Query Match             28.1%;  Score 460;  DB 13;  Length 289;
  Best Local Similarity   35.8%;  Pred. No. 7e-37;
  Matches  103;  Conservative   57;  Mismatches  108;  Indels   20;  Gaps    7;

Qy          27 CLIGAVNL---KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKI-QDEQTTYVFFDN 82
               | :  | |    : | | :|:| || || |  :    || ||:||| : :|::|::||:|
Db          18 CCLWTVTLAAVTTPNPTIIVKEGESAELQCSYSSDFTS-PRVEWKFVNKDQETSFVFYDG 76
```

```
Qy          83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTP 142
               :          || |      : :  :||:|:  | ||| :   :     |  |:| | | |  |
Db          77 SLTAPYKDRA-IPYPQGITLKQITRKDAGEYSCEVTSTGSKTLYGEAKIQLQVIVAPSKP 135

Qy         143 VCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETG 202
               | :||::|  | :| | | |::|:| | : |||| |:    :  |  :||:: :: :||
Db         136 VAQVPRSVSTGSVAELLCVENDGYPPPTFIWYRNKSPM----QIAP--QNSTYTIDPKTG 189

Qy         203 TLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLG 262
               | | ||   |||:||| |:|: |    :   |:| |:|:|||:  |::|| :|||  |
Db         190 VLKFAAVSTSDSGEYYCEATNNQGKQASDLVRMDVQDVNVGGIVAAVVIVLLILALIGFG 249

Qy         263 ICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               :  || |||    :     |  | :       |  : :|:  |||::
Db         250 MWFAYSRGYLDRKENKKVIYSLPSE--------TRSDKNFQQTSSFLV 289


RESULT 12
Q8VC39
ID   Q8VC39      PRELIMINARY;      PRT;   300 AA.
AC   Q8VC39;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Junction cell adhesion molecule1).
GN   F11R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; BC021876; AAH21876.1; -.
DR   EMBL; AK033574; BAC28369.1; -.
DR   MGD; MGI:1321398; F11r.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   300 AA;  32423 MW;  3CB561E8FF3B97EC CRC64;

  Query Match           27.9%;  Score 457.5;  DB 11;  Length 300;
  Best Local Similarity   35.6%;  Pred. No. 1.3e-36;
  Matches  106;  Conservative   56;  Mismatches  121;  Indels   15;  Gaps    7;

Qy          20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
               || ||   ::|::      :: ::     | | ||::|:|  | |  | ||:||| :|
Db          11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy          75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
               |  | ::::|     | |       : :   :|||:|:  | | :|:    :   |: | ||
Db          69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy         135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
               | | |   || :| :|  | | | | :| |   |||::: : : | |::    | ||
Db         127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy         194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
               || :: ::| |:|  |   |||:|||  | |  |:| | |   |:  :||:|||:  |||
Db         187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy         253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               | :| |:  |:  || ||||   |:        |||    :   |  ||:|:  |||::
Db         247 LILLGLLIFGVWFAYSRGYFERTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 13
Q7SYQ7
ID   Q7SYQ7      PRELIMINARY;      PRT;   300 AA.
AC   Q7SYQ7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054305; AAH54305.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   300 AA;  32858 MW;  02BC49DC74E271D4 CRC64;

  Query Match           26.9%;  Score 440.5;  DB 13;  Length 300;
  Best Local Similarity   34.7%;  Pred. No. 6.2e-35;
  Matches  103;  Conservative   55;  Mismatches  114;  Indels   25;  Gaps    7;

Qy          20 LLLLFRGCLIGA--VNLKSSNRTPVVQEFESVELSCIITDSQTSD---PRIEWKKI-QDE 73
               | ||   ||  |     : : :  |  |:| :| :| |     | |||   ||:||| : :|:
Db          23 LALLCCCCLWTAALAGVTAPDPTITVKEGDSPDLRC----SYTSDYINPRVEWKFVNKDQ 78

Qy          74 QTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIEL 133
```

```
                :|::||:|  :      ||    :  :|:  |||:|:  | |||  :   :    |  |:|
Db          79 ETSFVFYDGSLTASYKDRATSYPQ-GIKLNQVTRKDAGEYSCEVTSTGTKVLYGEAKIQL 137

Qy         134 TVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNS 193
                | | | ||| :|| :   | :| | | |::| | | ::|| |: |:   |       :||
Db         138 QVIVAPGTPVAQVPSSARTGSVAELMCVETQGFPLPTPTWYHNNSPMQAKS------QNS 191

Qy         194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVL 253
               :: ::  || | | :|   |||:||| |:|  |          |:| |:|:|||:  |::||
Db         192 TYTIDPNTGVLKFASVGTSDSGEYYCKATNSQGEQSSAIVRMDVKDVNVGGIVAAVVIVL 251

Qy         254 AVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
                :|||:  |:  || |||          | | :        |  : :|:  |||::
Db         252 LILALLGFGLWFAYSRGYLDRKGNKKVIYSQPSE--------TRSDKNFQQTSSFLV 300


RESULT 14
Q9Y5B2
ID   Q9Y5B2      PRELIMINARY;      PRT;   259 AA.
AC   Q9Y5B2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA   Foley C., Parkos C.A.;
RT   "Human junctional adhesion molecule is expressed by polarized columnar
RT   epithelia and regulates tight junction resealing.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF154005; AAD43794.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   259 AA;  28122 MW;  FE38521A911582D0 CRC64;

  Query Match             20.5%;  Score 336;  DB 4;  Length 259;
  Best Local Similarity   29.6%;  Pred. No. 1.1e-24;
  Matches   81;  Conservative   45;  Mismatches  110;  Indels   38;  Gaps    7;

Qy          42 VVQEPESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLK 101
               :: |   |:|||    |  | ||        ::: |::                  | :
Db          19 ILPENNPVKLSCAY--SGFSSPR---AASYEDRVTFL-----------------PTGIT 55

Qy         102 IWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQ 161
                 :||| |:  | | :|         |: ::| | | |   |   :| :  :|  | |.|
Db          56 FKSVTREDTGTYTC-MVFEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCS 114

Qy         162 ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA 221
               | :| |   |:|::: : :||: ::   | |||: ||  || |||  :   |:|:| | |
Db         115 EQDGSPPSEYTWFKDGIVMPTNPKSTRAPSNSSYVLNPTTGELVFDPLSASDTGEYSCEA 174

Qy         222 SNDAGSARCEEQ-EMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGE 280
                | |:          ||  : |:| |:  ||| | :| ::  ||  || ||:|   |:
Db         175 RNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTS 234

Qy         281 S----YKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               |    | |           ||:|:  |||::
Db         235 SKKVIYSQPS---------ARSEGEFKQTSSFLV 259


RESULT 15
Q9JKD5
ID   Q9JKD5      PRELIMINARY;      PRT;   173 AA.
AC   Q9JKD5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kirsch T., Wellner M., Haller H., Lippoldt A.;
RT   "Cloning of the rat junctional adhesion molecule (JAM).";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF241261; AAF61729.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
FT   NON_TER      1      1
SQ   SEQUENCE   173 AA;  18706 MW;  3EE3ECDFA5AFB8B2 CRC64;

  Query Match             19.9%;  Score 326;  DB 11;  Length 173;
  Best Local Similarity   40.3%;  Pred. No. 6.1e-24;
  Matches   71;  Conservative   28;  Mismatches   71;  Indels    6;  Gaps    3;

Qy         137 VKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNSSF 195
                | |  |   :| :| :|  | | | | :| |   |||::: ||: | |::    | |||:
Db           2 VPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAFINSSY 61

Qy         196 HLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVVLA 254
                 :: ::| |||   |   |||:||| | |  |:| | |   ||  :||:|||:  ||| |
Db          62 TIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVTLI 121

Qy         255 VLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               :| |:  ||  || ||||   |:       |||    :       ||:|:  |||::
Db         122 LLGLLIPGIWFAYSRGYFERTKKG----TAPGKKVIYSQPSARSEGEFKQTSSFLV 173


Search completed: June 15, 2004, 11:05:06
Job time : 37 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1637	100.0	310	4	US-09-907-794A-423	Sequence 423, App
2	1637	100.0	310	4	US-09-905-125A-423	Sequence 423, App
3	1637	100.0	310	4	US-09-902-775A-423	Sequence 423, App
4	481	29.4	298	4	US-09-152-060-76	Sequence 76, Appl
5	461.5	28.2	312	4	US-09-254-465A-9	Sequence 9, Appli
6	461.5	28.2	312	4	US-09-907-794A-64	Sequence 64, Appl
7	461.5	28.2	312	4	US-09-905-125A-64	Sequence 64, Appl
8	461.5	28.2	312	4	US-09-902-775A-64	Sequence 64, Appl
9	457.5	27.9	300	4	US-09-254-465A-10	Sequence 10, Appl
10	424	25.9	299	3	US-09-188-930-331	Sequence 331, App
11	424	25.9	299	4	US-09-462-270-2	Sequence 2, Appli
12	424	25.9	299	4	US-09-254-465A-1	Sequence 1, Appli
13	424	25.9	299	4	US-09-312-283C-189	Sequence 189, App
14	424	25.9	299	4	US-09-312-283C-331	Sequence 331, App
15	424	25.9	299	4	US-09-907-794A-119	Sequence 119, App
16	424	25.9	299	4	US-09-905-125A-119	Sequence 119, App
17	424	25.9	299	4	US-09-902-775A-119	Sequence 119, App
18	412	25.2	299	3	US-09-188-930-189	Sequence 189, App
19	392.5	24.0	260	4	US-09-254-465A-23	Sequence 23, Appl
20	392.5	24.0	263	4	US-09-254-465A-25	Sequence 25, Appl
21	288	17.6	205	4	US-09-462-270-4	Sequence 4, Appli
22	228.5	14.0	319	1	US-08-597-495B-22	Sequence 22, Appl
23	228.5	14.0	319	3	US-09-068-051A-22	Sequence 22, Appl
24	228.5	14.0	319	4	US-09-336-536-67	Sequence 67, Appl
25	228.5	14.0	319	4	US-09-254-465A-6	Sequence 6, Appli
26	217.5	13.3	270	4	US-09-254-465A-24	Sequence 24, Appl
27	217.5	13.3	273	4	US-09-254-465A-26	Sequence 26, Appl
28	215.5	13.2	318	3	US-09-068-051A-32	Sequence 32, Appl
29	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
30	173.5	10.6	370	4	US-09-336-536-28	Sequence 28, Appl
31	171.5	10.5	394	4	US-09-336-536-39	Sequence 39, Appl
32	169.5	10.4	390	2	US-08-979-424-1	Sequence 1, Appli
33	169.5	10.4	390	4	US-09-907-794A-39	Sequence 39, Appl
34	169.5	10.4	390	4	US-09-905-125A-39	Sequence 39, Appl
35	169.5	10.4	390	4	US-09-902-775A-39	Sequence 39, Appl
36	167	10.2	365	4	US-09-336-536-40	Sequence 40, Appl
37	166.5	10.2	341	4	US-09-336-536-29	Sequence 29, Appl
38	163.5	10.0	398	4	US-09-778-510-6	Sequence 6, Appli
39	163.5	10.0	398	4	US-09-907-794A-84	Sequence 84, Appl
40	163.5	10.0	398	4	US-09-905-125A-84	Sequence 84, Appl
41	163.5	10.0	398	4	US-09-902-775A-84	Sequence 84, Appl
42	162.5	9.9	246	4	US-09-336-536-31	Sequence 31, Appl
43	161	9.8	313	4	US-09-700-397-4	Sequence 4, Appli
44	161	9.8	344	4	US-09-700-397-3	Sequence 3, Appli
45	160.5	9.8	365	3	US-08-928-383B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

```
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-794A-423

  Query Match             100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-159;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-125A-423

  Query Match             100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-159;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
```

```
Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 3
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-775A-423

  Query Match             100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-159;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 4
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 28 Human Secreted Proteins
;  FILE REFERENCE: PZ003P1.US
;  CURRENT APPLICATION NUMBER: US/09/152,060
;  CURRENT FILING DATE: 1998-09-11
;  EARLIER APPLICATION NUMBER: PCT/US98/04858
;  EARLIER FILING DATE: 1998-03-12
;  EARLIER APPLICATION NUMBER: 60/040,762
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/040,710
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/050,934
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,100
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,357
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,189
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/057,765
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/048,970
```

```
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/068,368
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 298
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (42)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (58)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

  Query Match             29.4%;  Score 481;  DB 4;  Length 298;
  Best Local Similarity   35.8%;  Pred. No. 7.7e-41;
  Matches  114;  Conservative   60;  Mismatches  116;  Indels   28;  Gaps   10;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::      |    :      ||   ::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVKYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVN 292
              : |:| |||| |||  |:||  |:::  ||:| | |:||| :|:   |::   | :  :
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSS 280

Qy        293 YIRTDEEGDFRHKSSFVI 310
                |  | ||:|  ||:|
Db        281 KATTMSENDFKHTKSFII 298


RESULT 5
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 9
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-254-465A-9

  Query Match             28.2%;  Score 461.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 8.1e-39;
  Matches  104;  Conservative   52;  Mismatches  103;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::      |    :      ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
              : |:| |||| |||  |:||  |:::  ||:| | |:|||
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 6
US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
```

```
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-64

  Query Match             28.2%;  Score 461.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 8.1e-39;
  Matches  104;  Conservative   52;  Mismatches  103;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::       |    :     ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
              : |:| |||| |||  |:||  |:::  ||:| | |:|||
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 7
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-905-125A-64

  Query Match             28.2%;  Score 461.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 8.1e-39;
  Matches  104;  Conservative   52;  Mismatches  103;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::       |    :     ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
```

```
                 |  :|   |:||||:     ::|::   :|||   |||::   :::| ||||  |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
              : |:| |||| ||| |:||  |::: ||:| | |:|||
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 8
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-775A-64

  Query Match             28.2%;  Score 461.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 8.1e-39;
  Matches  104;  Conservative   52;  Mismatches  103;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EPESVELSC 53
              || |   ||          |||| |  ::      |    :     ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| ||||  |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||: :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
              : |:| |||| ||| |:||  |::: ||:| | |:|||
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 9
US-09-254-465A-10
; Sequence 10, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 10
;   LENGTH: 300
```

```
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-254-465A-10

  Query Match             27.9%;  Score 457.5;  DB 4;  Length 300;
  Best Local Similarity   35.6%;  Pred. No. 2e-38;
  Matches  106;  Conservative   56;  Mismatches  121;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEPESVELSCIITDSQTSDPRIEWKKIQDEQ 74
              || ||   ::|::     :: ::     | | ||::|:|  | |  | ||:||| :|
Db         11 LLPLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
              |  | ::::|    | |      : :   :|||:|:  | | :|:    :    |: | ||
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
              | | |  |   || :| :|  | | | | :| |   |||::: : : | |::    | ||
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
              || :: ::| |:|  |   |||:||| | |  |:| | |   |:  :||:|||:  |||
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              | :| |:  |:  || ||||   |:       |||    :   |  ||:|:  |||::
Db        247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 10
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Human
US-09-188-930-331

  Query Match             25.9%;  Score 424;  DB 3;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|    :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | :  |  | ::|||      |   |  :  :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||: ||  || |||   :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    | |              ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 11
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
;  APPLICANT:  SmithKline Beecham Corporation
;  TITLE OF INVENTION:  Human F11 Antigen: A Cell Surface
;  TITLE OF INVENTION:  Receptor   Involved in Platelet Aggregation
;  FILE REFERENCE:  GH-70150US
;  CURRENT APPLICATION NUMBER: US/09/462,270
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/052,186
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-462-270-2

  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|    :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | :  |  | ::|||      |   |  :  :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||: ||  || |||   :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    | |              ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Pong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
```

```
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 1
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-254-465A-1

  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   |  :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
                | |||: ||  || |||  :   |:|:| | | |  |:        ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    | |               ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 13
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-189

  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   |  :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
                | |||: ||  || |||  :   |:|:| | | |  |:        ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    | |               ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 14
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-331

  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   |  :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
                | |||: ||  || |||  :   |:|:| | | |  |:        ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                ||| | :| ::  ||  || ||:|   |:   |    | |               ||:|
```

```
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 15
US-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-119

  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 5.1e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTSDPRIEW 67
              |  ||      | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----PILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              | | : |  | ::|||      |   |  | :  :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |  :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||: ||  || |||  :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
              ||| | :| ::  ||  || ||:|   |:   |    | |                ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


Search completed: June 15, 2004, 11:06:32
Job time : 17.5 secs
```

PCT/US99/28313

~~20032224~~

20032221

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:50:54 ; Search time 51.5 Seconds
(without alignments)
1700.771 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1637	100.0	310	3	AAY96735	Aay96735 PRO1868,
2	1637	100.0	310	3	AAB33457	Aab33457 Human PRO
3	1637	100.0	310	3	AAB27276	Aab27276 Human con
4	1637	100.0	310	4	AAB80272	Aab80272 Human PRO
5	1637	100.0	310	4	AAM93905	Aam93905 Human pol
6	1637	100.0	310	4	AAM93323	Aam93323 Human pol
7	1637	100.0	310	4	AAU12440	Aau12440 Human PRO
8	1637	100.0	310	4	AAB80383	Aab80383 Secreted
9	1637	100.0	310	4	AAB80408	Aab80408 Secreted
10	1637	100.0	310	4	AAB80409	Aab80409 Secreted
11	1637	100.0	310	5	ABG92709	Abg92709 Human sec
12	1637	100.0	310	5	ABG91361	Abg91361 Novel hum
13	1637	100.0	310	5	ABB84947	Abb84947 Human PRO
14	1637	100.0	310	5	ABG65297	Abg65297 Human alb
15	1637	100.0	310	5	ABG65296	Abg65296 Human alb
16	1637	100.0	310	5	ABG65298	Abg65298 Human alb
17	1637	100.0	310	5	ABG31401	Abg31401 Human PRO
18	1637	100.0	310	5	ABB95553	Abb95553 Human ang
19	1637	100.0	310	6	ABU71650	Abu71650 Human PRO
20	1637	100.0	310	6	ABU72377	Abu72377 Novel hum
21	1637	100.0	310	6	ABU80867	Abu80867 Human sec
22	1637	100.0	310	6	ABO17884	Abo17884 Novel hum
23	1637	100.0	310	6	ABU71505	Abu71505 Human PRO
24	1637	100.0	310	6	ADA57610	Ada57610 Human sec
25	1637	100.0	310	6	ADA57611	Ada57611 Human sec
26	1637	100.0	310	6	ADA57309	Ada57309 Human sec
27	1637	100.0	310	6	ABP71277	Abp71277 Human jun
28	1637	100.0	310	6	ABU81138	Abu81138 Human PRO
29	1637	100.0	310	6	ABU71951	Abu71951 Human sec
30	1637	100.0	310	6	ABO01834	Abo01834 Novel hum
31	1637	100.0	310	6	ABU66838	Abu66838 Human PRO
32	1637	100.0	310	6	ABU54407	Abu54407 Human sec
33	1637	100.0	310	6	ABO47422	Abo47422 Human sec
34	1637	100.0	310	6	ABG73314	Abg73314 Human PRO
35	1637	100.0	310	6	ABU59919	Abu59919 Novel sec
36	1637	100.0	310	6	ABO25109	Abo25109 Human sec
37	1637	100.0	310	6	ABU64559	Abu64559 Human sec
38	1637	100.0	310	6	ABU67405	Abu67405 Human sec
39	1637	100.0	310	6	ABO14925	Abo14925 Human sec
40	1637	100.0	310	6	ABU60813	Abu60813 Human sec
41	1637	100.0	310	6	ABU67114	Abu67114 Human sec
42	1637	100.0	310	6	ABU81236	Abu81236 Human PRO
43	1637	100.0	310	6	ABU69682	Abu69682 Novel hum
44	1637	100.0	310	6	ABO14864	Abo14864 Human sec
45	1637	100.0	310	6	ADA46057	Ada46057 Novel hum

ALIGNMENTS

RESULT 1
AAY96735
ID AAY96735 standard; protein; 310 AA.
XX
AC AAY96735;
XX
DT 26-SEP-2000 (first entry)
XX
DE PRO1868, an A33 antigen homologue.
XX
KW PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .30
FT /label= Signal_peptide
FT Modified-site 26. .31
FT /note= "N-myristoylation site"
FT Modified-site 69. .77
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 104. .107
FT /note= "N-glycosylation site"
FT Modified-site 106. .109
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 107. .110
FT /note= "cAMP- and cGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 192. .195
FT /note= "N-glycosylation site"
FT Modified-site 215. .220
FT /note= "N-myristoylation site"
FT Modified-site 226. .231
FT /note= "N-myristoylation site"
FT Domain 243. .263
FT /label= Transmembrane_domain
FT Modified-site 243. .248
FT /note= "N-myristoylation site"
FT Modified-site 244. .249
FT /note= "N-myristoylation site"
FT Modified-site 262. .267
FT /note= "N-myristoylation site"
FT Modified-site 296. .299
FT /note= "Casein kinase II phosphorylation site"
XX
PN WO200036102-A2.
XX

```
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028634.
XX
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI   Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51265.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide.
XX
PS   Claim 1; Fig 14; 154pp; English.
XX
CC   This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC   cancer-associated marker. The invention concerns novel secreted and
CC   transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC   sequences are useful in the recombinant production of PRO polypeptides,
CC   as a hybridization probe to screen libraries to isolate cDNAs with
CC   sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC   polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC   used to produce transgenic animals useful for the development and
CC   screening of therapeutically useful reagents. They can also be used in
CC   gene therapy, e.g. to replace a defective gene
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1637;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
AAB33457
ID   AAB33457 standard; protein; 310 AA.
XX
AC   AAB33457;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US005841.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-MAR-1999;   99US-0123957P.
PR   23-MAR-1999;   99US-0125775P.
PR   12-APR-1999;   99US-0128849P.
PR   20-APR-1999;   99WO-US008615.
PR   28-APR-1999;   99US-0131445P.
PR   04-MAY-1999;   99US-0132371P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
```

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58622.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 88; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 3
AAB27276
ID AAB27276 standard; protein; 310 AA.
XX
AC AAB27276;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #2.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA95306.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
AAB80272
ID AAB80272 standard; protein; 310 AA.
XX
AC AAB80272;
XX
DT 24-APR-2001 (first entry)

XX
DE Human PRO1868 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR N-PSDB; AAP72433.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
PS Claim 1; Fig 124; 393pp; English.
XX
CC The present sequence is one of sixty one novel secreted and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful for treating skin
CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
AAM93905
ID AAM93905 standard; protein; 310 AA.
XX
AC AAM93905;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 4051.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94867.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO

```
XX
SQ   Sequence 310 AA;

  Query Match           100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
AAM93323
ID   AAM93323 standard; protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94243.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match           100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
AAU12440
ID   AAU12440 standard; protein; 310 AA.
XX
AC   AAU12440;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO1868 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
```

PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21512.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 538; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 8
AAB80383
ID AAB80383 standard; protein; 310 AA.
XX
AC AAB80383;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #13.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 538-539; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

```
  Query Match           100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 9
AAB80408
ID AAB80408 standard; protein; 310 AA.
XX
AC AAB80408;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #38.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

```
  Query Match           100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 10
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or

```
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. Also used in food
CC   preparations
XX
SQ   Sequence 310 AA;

  Query Match            100.0%;  Score 1637;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 11
ABG92709
ID   ABG92709 standard; protein; 310 AA.
XX
AC   ABG92709;
XX
DT   18-NOV-2002  (first entry)
XX
DE   Human secreted protein PRO1868.
XX
KW   Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW   PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW   inflammatory disorder; immune related disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW   autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW   psoriasis; allergic disease of the lung; graft-versus host disease;
KW   tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002098506-A1.
XX
PD   25-JUL-2002.
XX
PF   27-DEC-2001; 2001US-00033301.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-690475/74.
DR   N-PSDB; ABS68392.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides useful
PT   for diagnosis and treatment of inflammatory disorders and immune-related
PT   diseases, and identifying modulators.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to an isolated polypeptide having at least 80%
CC   amino acid sequence identity to secreted and transmembrane polypeptides
CC   PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC   PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC   cells and antibodies against PRO polypeptides. PRO proteins are useful
CC   for identifying modulators of the polypeptide. PRO1868 useful for the
CC   diagnosis and treatment of inflammatory and immune related diseases
CC   including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC   sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC   infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC   versus host disease and tumours. Pro nucleic acids are useful for
CC   constructing hybridisation probes for mapping the gene that encodes that
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   and for generating transgenic animals which are useful in the development
CC   and screening of therapeutically useful reagents. PRO nucleic acids are
CC   also useful for gene therapy, chromosome identification, and tissue
CC   typing. PRO proteins are useful as molecular weight markers for protein
CC   electrophoresis purposes. The anti-PRO antibodies are useful in
CC   diagnostic assays for PRO, e.g. detecting its expression in specific
CC   cells, tissues or serum and for affinity purification of PRO. The present
CC   sequence represents a PRO protein
XX
SQ   Sequence 310 AA;

  Query Match            100.0%;  Score 1637;  DB 5;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
ABG91361
ID ABG91361 standard; protein; 310 AA.
XX
AC ABG91361;
XX
DT 29-NOV-2002 (first entry)
XX
DE Novel human secreted protein #7.
XX
KW Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW immunogenic.
XX
OS Homo sapiens.
XX
PN US2002098505-A1.
XX
PD 25-JUL-2002.
XX
PF 28-DEC-2001; 2001US-00033246.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-665999/71.
DR N-PSDB; ABS67460.
XX
PT New human secreted and transmembrane (PRO) polypeptides, useful for
PT treating conditions requiring PRO polypeptides, for screening PRO
PT antagonists and agonists useful as drug candidates.
XX
PS Claim 12; Fig 14; 125pp; English.
XX
CC The invention relates to new human secreted and transmembrane proteins
CC (PRO) and nucleic acids of the invention. The polypeptides can be
CC administered therapeutically, especially by expressing encoding
CC polynucleotides, e.g. in therapeutic compositions. They can be used to
CC screen for PRO polypeptide antagonists and agonists useful to identify
CC drug candidates. They can also be used to produce antibodies, useful to
CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC therapeutically (e.g. as antagonists or to target and/or deliver
CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC produce antisense sequences to inhibit polypeptide production. They can
CC be used to produce probes and primers useful to detect or isolate
CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC sequences from other species. They are also useful for gene mapping and
CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC amino acid sequences of the invention
XX
SQ Sequence 310 AA;

```
  Query Match           100.0%;  Score 1637;  DB 5;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 13
ABB84947
ID ABB84947 standard; protein; 310 AA.
XX
AC ABB84947;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1868 protein sequence SEQ ID NO:262.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.

```
PR   20-JUL-2000; 2000US-0219556P.
PR   25-JUL-2000; 2000US-0220624P.
PR   25-JUL-2000; 2000US-0220664P.
PR   28-JUL-2000; 2000WO-US020710.
PR   02-AUG-2000; 2000US-0222695P.
PR   17-AUG-2000; 2000US-00643657.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   07-SEP-2000; 2000US-0230978P.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   24-OCT-2000; 2000US-0242922P.
PR   08-NOV-2000; 2000US-00709238.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   22-JAN-2001; 2001US-00767609.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   30-MAY-2001; 2001US-00870574.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   N-PSDB; ABL88202.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal.
XX
PS   Claim 11; Fig 262; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC   cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The PRO polynucleotides have applications in molecular biology,
CC   including use as hybridisation probes, and in chromosome and gene
CC   mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC   exemplification of the present invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1637;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 14
ABG65297
ID   ABG65297 standard; protein; 310 AA.
XX
AC   ABG65297;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human albumin fusion protein #1972.
XX
KW   Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW   human serum albumin; HSA; cancer; reproductive disorder;
KW   digestive disorder; immune disorder; endocrine disorder;
KW   haematopoietic disorder; neural disorder; connective disorder;
KW   cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW   immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW   neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW   osteopathic; antiarthritic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177137-A1.
XX
PD   18-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011988.
XX
PR   12-APR-2000; 2000US-0229358P.
PR   25-APR-2000; 2000US-0199384P.
PR   21-DEC-2000; 2000US-0256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2002-010886/01.
XX
PT   New fusion protein for treating disease e.g. diabetes comprises an
PT   albumin fused to a therapeutic protein.
XX
PS   Claim 1; Page 1895; 2102pp; English.
XX
CC   The present invention relates to albumin fusion proteins comprising a
CC   therapeutic protein X and human albumin (HA, also known as human serum
CC   albumin, HSA). The proteins are useful for treating a disease or disorder
CC   that may be modulated by therapeutic protein X. The albumin extends the
CC   shelf-life of protein X, and may increase its biological in vitro/in vivo
CC   activity. The protein is useful for treating and diagnosing disorders
CC   such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
```

```
CC   disease, ulcerative colitis), immune disorders (e.g. acquired
CC   immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC   haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC   Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC   schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC   ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1637;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
ABG65296
ID   ABG65296 standard; protein; 310 AA.
XX
AC   ABG65296;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human albumin fusion protein #1971.
XX
KW   Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW   human serum albumin; HSA; cancer; reproductive disorder;
KW   digestive disorder; immune disorder; endocrine disorder;
KW   haematopoietic disorder; neural disorder; connective disorder;
KW   cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW   immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW   neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW   osteopathic; antiarthritic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177137-A1.
XX
PD   18-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011988.
XX
PR   12-APR-2000; 2000US-0229358P.
PR   25-APR-2000; 2000US-0199384P.
PR   21-DEC-2000; 2000US-0256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2002-010886/01.
XX
PT   New fusion protein for treating disease e.g. diabetes comprises an
PT   albumin fused to a therapeutic protein.
XX
PS   Claim 1; Page 1893-1894; 2102pp; English.
XX
CC   The present invention relates to albumin fusion proteins comprising a
CC   therapeutic protein X and human albumin (HA, also known as human serum
CC   albumin, HSA). The proteins are useful for treating a disease or disorder
CC   that may be modulated by therapeutic protein X. The albumin extends the
CC   shelf-life of protein X, and may increase its biological in vitro/in vivo
CC   activity. The protein is useful for treating and diagnosing disorders
CC   such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC   disease, ulcerative colitis), immune disorders (e.g. acquired
CC   immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC   haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC   Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC   schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC   ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1637;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: June 15, 2004, 11:03:07
Job time : 52.5 secs
```

3/4/2000 1999 -013

3/13/2000 → SEQ ID NO: 15

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:45 ; Search time 51 Seconds
(without alignments)
1717.446 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHPFL.....VNYIRTSEEGDFRHKSSPVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	3	AAB27278	Aab27278 Murine co
2	310	100.0	310	3	AAB27272	Aab27272 Human con
3	24	7.7	285	3	AAB39254	Aab39254 Human sec
4	24	7.7	291	4	ABG04645	Abg04645 Novel hum
5	24	7.7	310	3	AAY96294	Aay96294 Human IGF
6	24	7.7	310	3	AAY96735	Aay96735 PRO1868,
7	24	7.7	310	3	AAB33457	Aab33457 Human PRO
8	24	7.7	310	3	AAB27276	Aab27276 Human con
9	24	7.7	310	4	AAB80272	Aab80272 Human PRO
10	24	7.7	310	4	AAM93905	Aam93905 Human pol
11	24	7.7	310	4	AAM93323	Aam93323 Human pol
12	24	7.7	310	4	AAU12440	Aau12440 Human PRO
13	24	7.7	310	4	AAB80383	Aab80383 Secreted
14	24	7.7	310	4	AAB80408	Aab80408 Secreted
15	24	7.7	310	4	AAB80409	Aab80409 Secreted
16	24	7.7	310	5	ABG92709	Abg92709 Human sec
17	24	7.7	310	5	ABG91361	Abg91361 Novel hum
18	24	7.7	310	5	ABB84947	Abb84947 Human PRO
19	24	7.7	310	5	ABG65297	Abg65297 Human alb
20	24	7.7	310	5	ABG65296	Abg65296 Human alb
21	24	7.7	310	5	ABG65298	Abg65298 Human alb
22	24	7.7	310	5	ABG31401	Abg31401 Human PRO
23	24	7.7	310	5	ABB95553	Abb95553 Human ang
24	24	7.7	310	6	ABU71650	Abu71650 Human PRO
25	24	7.7	310	6	ABU72377	Abu72377 Novel hum
26	24	7.7	310	6	ABU80867	Abu80867 Human sec
27	24	7.7	310	6	ABO17884	Abo17884 Novel hum
28	24	7.7	310	6	ABU71505	Abu71505 Human PRO
29	24	7.7	310	6	ADA57610	Ada57610 Human sec
30	24	7.7	310	6	ADA57611	Ada57611 Human sec
31	24	7.7	310	6	ADA57309	Ada57309 Human sec
32	24	7.7	310	6	ABP71277	Abp71277 Human jun
33	24	7.7	310	6	ABU81138	Abu81138 Human PRO
34	24	7.7	310	6	ABU71951	Abu71951 Human sec
35	24	7.7	310	6	ABO01834	Abo01834 Novel hum
36	24	7.7	310	6	ABU66838	Abu66838 Human PRO
37	24	7.7	310	6	ABU54407	Abu54407 Human sec
38	24	7.7	310	6	ABO47422	Abo47422 Human sec
39	24	7.7	310	6	ABG73314	Abg73314 Human PRO
40	24	7.7	310	6	ABU59919	Abu59919 Novel sec
41	24	7.7	310	6	ABO25109	Abo25109 Human sec
42	24	7.7	310	6	ABU64559	Abu64559 Human sec
43	24	7.7	310	6	ABU67405	Abu67405 Human sec
44	24	7.7	310	6	ABO14925	Abo14925 Human sec
45	24	7.7	310	6	ABU60813	Abu60813 Human sec

ALIGNMENTS

RESULT 1
AAB27278
ID AAB27278 standard; protein; 310 AA.
XX
AC AAB27278;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine confluency regulated adhesion molecule 1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; mouse;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Mus sp.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA97189.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Example; Fig 8; 59pp; English.
XX
CC The present sequence is the murine confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-288;

```
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 2
AAB27272
ID AAB27272 standard; protein; 310 AA.
XX
AC AAB27272;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 1; Fig 3; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

```
  Query Match             100.0%;  Score 310;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-288;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 3
AAB39254
ID AAB39254 standard; protein; 285 AA.
XX
AC AAB39254;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis;
KW hyperproliferative disorder; cardiovascular disorder; infection;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; chemotaxis.
XX
OS Homo sapiens.
XX
PN WO200056754-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US006792.
XX
PR 19-MAR-1999; 99US-0125362P.
PR 10-DEC-1999; 99US-0169980P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen GA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-579483/54.
DR N-PSDB; AAC74237.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 32; 434pp; English.
XX
CC The polynucleotide sequences given in AAC74223-C74279 encode the human
CC secreted proteins represented in AAB39179-B39226. Sequences AAB39227-
CC B39308 are alternative proteins encoded by the genes, and also protein
CC sequences with which they share homology. The proteins have activities

CC based on the tissues and cells in which they are expressed. Examples of
CC activities include: immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
CC nootropic; neuroprotective; antibacterial; virucide; fungicide; and
CC opthalmalogical. The human secreted proteins, polynucleotides,
CC antagonists and agonists of the invention may be useful in the treatment,
CC prevention, and/or diagnosis of various disease, disorders and conditions
CC such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to regenerate tissues,
CC maintain organs before transplantation, in chemotaxis and as a food
CC additive or preservative e.g. to increase storage capabilities. Sequences
CC AAC74214-C74222 and AAB39178 are used during the isolation and
CC characterisation of the genes of the invention
XX
SQ Sequence 285 AA;

Query Match 7.7%; Score 24; DB 3; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 142 PRPHYSWYRNDVPLPTDSRANPRF 165

RESULT 4
ABG04645
ID ABG04645 standard; protein; 291 AA.
XX
AC ABG04645;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #4636.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS68832.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 35004; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 291 AA;

Query Match 7.7%; Score 24; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 214 PRPHYSWYRNDVPLPTDSRANPRF 237

RESULT 5
AAY96294
ID AAY96294 standard; protein; 310 AA.
XX
AC AAY96294;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-6 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .30
FT /label= signal_peptide
FT Protein 31. .310
FT /label= IGFAM-6
FT Domain 46. .117
FT /label= Ig_domain
FT Domain 153. .221
FT /label= Ig_domain
FT Domain 238. .260
FT /label= transmembrane_domain
XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.
XX
PF 19-NOV-1999; 99WO-US027566.
XX
PR 19-NOV-1998; 98US-00195853.
PR 22-DEC-1998; 98US-0113635P.
PR 07-APR-1999; 99US-0128194P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lal P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27386.
XX

```
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders.
XX
PS   Claim 1; Page 82-83; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is
CC   expressed in reproductive, nervous and cardiovascular tissue, where
CC   cancer and inflammation are common. The gene, protein, its antibodies,
CC   agonists and antagonists are suitable for diagnosing and treating many
CC   diseases, including cancer, immune system disorders (such as
CC   inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,
CC   atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,
CC   emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,
CC   rheumatoid arthritis, scleroderma, systemic lupus erythematosus and
CC   ulcerative colitis), complications of cancer, haemodialysis and
CC   extracorporeal circulation, trauma and haematopoietic cancer (such as
CC   leukaemia) and infections caused by bacteria, viruses, fungi or parasites
XX
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 6
AAY96735
ID   AAY96735 standard; protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .30
FT                   /label= Signal_peptide
FT   Modified-site   26. .31
FT                   /note= "N-myristoylation site"
FT   Modified-site   69. .77
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   104. .107
FT                   /note= "N-glycosylation site"
FT   Modified-site   106. .109
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   107. .110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   192. .195
FT                   /note= "N-glycosylation site"
FT   Modified-site   215. .220
FT                   /note= "N-myristoylation site"
FT   Modified-site   226. .231
FT                   /note= "N-myristoylation site"
FT   Domain          243. .263
FT                   /label= Transmembrane_domain
FT   Modified-site   243. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   244. .249
FT                   /note= "N-myristoylation site"
FT   Modified-site   262. .267
FT                   /note= "N-myristoylation site"
FT   Modified-site   296. .299
FT                   /note= "Casein kinase II phosphorylation site"
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028634.
XX
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51265.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide.
XX
PS   Claim 1; Fig 14; 154pp; English.
XX
CC   This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC   cancer-associated marker. The invention concerns novel secreted and
CC   transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC   sequences are useful in the recombinant production of PRO polypeptides,
CC   as a hybridization probe to screen libraries to isolate cDNAs with
CC   sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC   polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC   used to produce transgenic animals useful for the development and
CC   screening of therapeutically useful reagents. They can also be used in
CC   gene therapy, e.g. to replace a defective gene
XX
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 7
AAB33457
ID   AAB33457 standard; protein; 310 AA.
XX
AC   AAB33457;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
```

KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58622.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 88; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 8
AAB27276
ID AAB27276 standard; protein; 310 AA.
XX
AC AAB27276;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #2.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA95306.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing

```
XX
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 9
AAB80272
ID   AAB80272 standard; protein; 310 AA.
XX
AC   AAB80272;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human PRO1868 protein.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
PF   22-FEB-2000; 2000WO-US004414.
XX
PR   07-JUL-1999;   99US-0143048P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000;  2000WO-US000219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N;
PI   Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ,  Kljavin IJ;
PI   Mather JP,  Pan J,  Paoni NF,  Roy MA,  Stewart TA,  Tumas D;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-081051/09.
DR   N-PSDB; AAF72433.
XX
PT   Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT   treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT   cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT   disease).
XX
PS   Claim 1; Fig 124; 393pp; English.
XX
CC   The present sequence is one of sixty one novel secreted and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful for treating skin
CC   diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC   gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC   diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC   cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC   ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC   disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC   infertility, AIDS and diabetes and retinal disorders such as retinitis
CC   pigmentosum. The PRO nucleic acids have applications in molecular
CC   biology, including use as hybridization probes, and in chromosome and
CC   gene mapping
XX
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 10
AAM93905
ID   AAM93905 standard; protein; 310 AA.
XX
AC   AAM93905;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 4051.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94867.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
```

```
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 11
AAM93323
ID   AAM93323 standard; protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94243.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 12
AAU12440
ID   AAU12440 standard; protein; 310 AA.
XX
AC   AAU12440;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO1868 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21512.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
```

PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 538; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 13
AAB80383
ID AAB80383 standard; protein; 310 AA.
XX
AC AAB80383;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #13.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 538-539; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 14
AAB80408
ID AAB80408 standard; protein; 310 AA.
XX
AC AAB80408;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #38.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190
```

RESULT 15
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

```
  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190
```

Search completed: June 15, 2004, 11:09:56
Job time : 51 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:08:05 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	7.7	310	4	US-09-907-794A-423	Sequence 423, App
2	24	7.7	310	4	US-09-905-125A-423	Sequence 423, App
3	24	7.7	310	4	US-09-902-775A-423	Sequence 423, App
4	8	2.6	48	1	US-08-485-455D-65	Sequence 65, Appl
5	8	2.6	48	2	US-08-482-130C-65	Sequence 65, Appl
6	8	2.6	48	2	US-08-484-211C-65	Sequence 65, Appl
7	8	2.6	48	3	US-08-906-769-65	Sequence 65, Appl
8	8	2.6	48	3	US-08-906-616-65	Sequence 65, Appl
9	8	2.6	48	3	US-08-817-795-65	Sequence 65, Appl
10	8	2.6	48	3	US-08-485-443B-65	Sequence 65, Appl
11	8	2.6	48	3	US-08-639-075A-65	Sequence 65, Appl
12	8	2.6	48	3	US-09-012-431-65	Sequence 65, Appl
13	8	2.6	48	3	US-09-012-692-65	Sequence 65, Appl
14	8	2.6	48	3	US-08-906-613-65	Sequence 65, Appl
15	8	2.6	48	5	PCT-US95-14442A-65	Sequence 65, Appl
16	8	2.6	208	4	US-09-134-001C-3209	Sequence 3209, Ap
17	8	2.6	246	3	US-08-906-769-127	Sequence 127, App
18	8	2.6	246	3	US-08-906-616-127	Sequence 127, App
19	8	2.6	246	3	US-08-639-075A-127	Sequence 127, App
20	8	2.6	246	3	US-09-012-431-127	Sequence 127, App
21	8	2.6	246	3	US-09-012-692-127	Sequence 127, App
22	8	2.6	246	3	US-08-906-613-127	Sequence 127, App
23	8	2.6	421	4	US-09-252-991A-30177	Sequence 30177, A
24	8	2.6	530	4	US-09-252-991A-28311	Sequence 28311, A
25	7	2.3	24	4	US-10-053-485-34	Sequence 34, Appl
26	7	2.3	107	4	US-08-999-689A-25	Sequence 25, Appl
27	7	2.3	147	4	US-09-252-991A-26005	Sequence 26005, A
28	7	2.3	170	3	US-09-189-035-2	Sequence 2, Appli
29	7	2.3	170	3	US-09-382-086-2	Sequence 2, Appli
30	7	2.3	227	4	US-09-252-991A-30173	Sequence 30173, A
31	7	2.3	230	4	US-09-252-991A-20017	Sequence 20017, A
32	7	2.3	249	2	US-09-154-802-1	Sequence 1, Appli
33	7	2.3	249	3	US-09-373-029-1	Sequence 1, Appli
34	7	2.3	293	4	US-09-252-991A-29543	Sequence 29543, A
35	7	2.3	303	4	US-09-252-991A-28605	Sequence 28605, A
36	7	2.3	372	4	US-09-252-991A-32717	Sequence 32717, A
37	7	2.3	410	4	US-09-252-991A-25451	Sequence 25451, A
38	7	2.3	411	4	US-09-252-991A-23711	Sequence 23711, A
39	7	2.3	450	4	US-09-252-991A-20555	Sequence 20555, A
40	7	2.3	489	4	US-09-134-001C-5241	Sequence 5241, Ap
41	7	2.3	503	4	US-09-134-001C-3948	Sequence 3948, Ap
42	7	2.3	526	4	US-09-107-532A-7127	Sequence 7127, Ap
43	7	2.3	539	4	US-09-252-991A-21539	Sequence 21539, A
44	7	2.3	547	4	US-09-252-991A-18576	Sequence 18576, A
45	7	2.3	659	4	US-09-252-991A-19154	Sequence 19154, A

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 3
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

```
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;    LENGTH: 310
;    TYPE: PRT
;    ORGANISM: Homo Sapien
US-09-902-775A-423

  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 4
US-08-485-455D-65
; Sequence 65, Application US/08485455D
; Patent No. 5712143
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary L.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,455D
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-455D-65

  Query Match             2.6%;  Score 8;  DB 1;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 5
US-08-482-130C-65
; Sequence 65, Application US/08482130C
; Patent No. 5962257
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary L.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,130C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1-1
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-482-130C-65

  Query Match             2.6%;  Score 8;  DB 2;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 6
US-08-484-211C-65
; Sequence 65, Application US/08484211C
; Patent No. 5972645
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary L.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,211C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-484-211C-65

  Query Match             2.6%;  Score 8;  DB 2;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 7
US-08-906-769-65
; Sequence 65, Application US/08906769
; Patent No. 6077687
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,769
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/639,075
;      FILING DATE:  24-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-906-769-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 8
US-08-906-616-65
; Sequence 65, Application US/08906616
; Patent No. 6121035
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
```

```
;       STREET:  1700 Lincoln Street, Suite 3500
;       CITY:  Denver
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80203
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/906,616
;       FILING DATE:  05-AUG-1997
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Connell, Gary J.
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:  2618-25-C2-3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 863-9700
;       TELEFAX:  (303) 863-0223
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  48 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-906-616-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 9
US-08-817-795-65
; Sequence 65, Application US/08817795
; Patent No. 6139840
;  GENERAL INFORMATION:
;     APPLICANT:  Grieve, Robert B.
;     APPLICANT:  Rushlow, Keith E.
;     APPLICANT:  Hunter, Shirley Wu
;     APPLICANT:  Frank, Glenn R.
;     APPLICANT:  Heath, Andrew W.
;     APPLICANT:  Yamaka, Miles Yamanaka
;     APPLICANT:  Arfsten, Ann
;     APPLICANT:  Dale, Beverly
;     APPLICANT:  Stiegler, Gary
;     TITLE OF INVENTION:  USE OF PROTEASE INHIBITORS AND
;     TITLE OF INVENTION:  PROTEASE VACCINES TO PROTECT  ANIMALS FROM FLEA
;     TITLE OF INVENTION:  INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
;     TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;     NUMBER OF SEQUENCES:  119
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sheridan Ross & McIntosh
;       STREET:  1700 Lincoln Street, Suite 3500
;       CITY:  Denver
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80203
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/817,795
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14442
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Gary J. Connell
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 863-9700
;       TELEFAX:  (303 863-0223
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  48 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-817-795-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 10
US-08-485-443B-65
; Sequence 65, Application US/08485443B
; Patent No. 6146870
;  GENERAL INFORMATION:
;     APPLICANT:  Grieve, Robert B.
;     APPLICANT:  Rushlow, Keith E.
;     APPLICANT:  Hunter, Shirley Wu
;     APPLICANT:  Frank, Glenn R.
;     APPLICANT:  Stiegler, Gary L.
;     TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;     TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;     NUMBER OF SEQUENCES:  79
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SHERIDAN ROSS
;       STREET:  1700 LINCOLN ST., SUITE 3500
;       CITY:  DENVER
;       STATE:  CO
;       COUNTRY:  USA
;       ZIP:  80203
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/485,443B
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Connell, Gary L.
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:  2618-25-C1-2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  303 863-9700
;       TELEFAX:  303 863-0223
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  48 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-485-443B-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 11
US-08-639-075A-65
; Sequence 65, Application US/08639075A
; Patent No. 6150125
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/639,075A
;      FILING DATE:  24-APR-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-639-075A-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 12
US-09-012-431-65
; Sequence 65, Application US/09012431
; Patent No. 6180383
;   GENERAL INFORMATION:
;        APPLICANT: Grieve, Robert B.
;                   Rushlow, Keith E.
;                   Wu Hunter, Shirley
;                   Frank, Glenn R.
;                   Stiegler, Gary
;                   Gaines, Patrick J.
;                   Silver, Gary
;        TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
;                            MOLECULES AND USES THEREOF
;        NUMBER OF SEQUENCES: 190
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Sheridan Ross & McIntosh
;             STREET: 1700 Lincoln Street, Suite 3500
;             CITY: Denver
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80203
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/012,431
;             FILING DATE: 23-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/639,075
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Connell, Gary J.
;             REGISTRATION NUMBER: 32,020
;             REFERENCE/DOCKET NUMBER: 2618-25-C2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (303) 863-9700
;             TELEFAX: (303) 863-0223
;   INFORMATION FOR SEQ ID NO: 65:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 48 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-012-431-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 13
US-09-012-692-65
; Sequence 65, Application US/09012692
; Patent No. 6214579
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/012,692
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/639,075
;       FILING DATE:  24-APR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Connell, Gary J.
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:  2618-25-C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 863-9700
;       TELEFAX:  (303) 863-0223
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  48 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-012-692-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 14
US-08-906-613-65
; Sequence 65, Application US/08906613
; Patent No. 6232096
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,613
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/639,075
;      FILING DATE:  24-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-906-613-65

  Query Match             2.6%;  Score 8;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
Db          1 VLIVLAVI 8


RESULT 15
PCT-US95-14442A-65
; Sequence 65, Application PC/TUS9514442A
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Hunter, Shirley Wu
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Heath, Andrew W.
;    APPLICANT:  Yamaka, Miles Yamanaka
;    APPLICANT:  Arfsten, Ann
;    APPLICANT:  Dale, Beverly
;    APPLICANT:  Stiegler, Gary
;    TITLE OF INVENTION:  USE OF PROTEASE INHIBITORS AND
;    TITLE OF INVENTION:  PROTEASE VACCINES TO PROTECT  ANIMALS FROM FLEA
;    TITLE OF INVENTION:  INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  119
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14442A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gary J. Connell
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-14442A-65

  Query Match             2.6%;  Score 8;  DB 5;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAVI 259
              ||||||||
```

Db 1 VLIVLAVI 8

Search completed: June 15, 2004, 11:13:22
Job time : 17.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:10:00 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1158786 seqs, 281726120 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	7.7	238	15	US-10-410-842A-18	Sequence 18, Appl
2	24	7.7	310	9	US-09-909-320-423	Sequence 423, App
3	24	7.7	310	9	US-09-909-088B-423	Sequence 423, App
4	24	7.7	310	9	US-09-905-291A-423	Sequence 423, App
5	24	7.7	310	9	US-09-902-853-423	Sequence 423, App
6	24	7.7	310	9	US-09-907-824-423	Sequence 423, App
7	24	7.7	310	9	US-09-907-841-423	Sequence 423, App
8	24	7.7	310	10	US-09-904-011-423	Sequence 423, App
9	24	7.7	310	10	US-09-906-742-423	Sequence 423, App
10	24	7.7	310	10	US-09-906-838-423	Sequence 423, App
11	24	7.7	310	10	US-09-907-613-423	Sequence 423, App
12	24	7.7	310	10	US-09-907-942-423	Sequence 423, App
13	24	7.7	310	10	US-09-904-859-423	Sequence 423, App
14	24	7.7	310	10	US-09-909-204-423	Sequence 423, App
15	24	7.7	310	10	US-09-904-820-423	Sequence 423, App
16	24	7.7	310	10	US-09-904-786-423	Sequence 423, App
17	24	7.7	310	10	US-09-906-646-423	Sequence 423, App
18	24	7.7	310	10	US-09-906-700-423	Sequence 423, App
19	24	7.7	310	10	US-09-903-786-423	Sequence 423, App
20	24	7.7	310	10	US-09-902-903-423	Sequence 423, App
21	24	7.7	310	10	US-09-903-749A-423	Sequence 423, App
22	24	7.7	310	10	US-09-904-119-423	Sequence 423, App
23	24	7.7	310	10	US-09-904-956-423	Sequence 423, App
24	24	7.7	310	10	US-09-902-736-423	Sequence 423, App
25	24	7.7	310	10	US-09-907-794-423	Sequence 423, App
26	24	7.7	310	10	US-09-903-943-423	Sequence 423, App
27	24	7.7	310	10	US-09-904-462-423	Sequence 423, App
28	24	7.7	310	10	US-09-907-925-423	Sequence 423, App
29	24	7.7	310	10	US-09-902-692-423	Sequence 423, App
30	24	7.7	310	10	US-09-903-520-423	Sequence 423, App
31	24	7.7	310	10	US-09-905-056-423	Sequence 423, App
32	24	7.7	310	10	US-09-909-064-423	Sequence 423, App
33	24	7.7	310	10	US-09-904-553-423	Sequence 423, App
34	24	7.7	310	10	US-09-905-381-423	Sequence 423, App
35	24	7.7	310	10	US-09-905-088-423	Sequence 423, App
36	24	7.7	310	10	US-09-907-575-423	Sequence 423, App
37	24	7.7	310	10	US-09-905-075-423	Sequence 423, App
38	24	7.7	310	10	US-09-902-759-423	Sequence 423, App
39	24	7.7	310	10	US-09-902-634-423	Sequence 423, App
40	24	7.7	310	10	US-09-902-713-423	Sequence 423, App
41	24	7.7	310	10	US-09-907-979-423	Sequence 423, App
42	24	7.7	310	10	US-09-902-615-423	Sequence 423, App
43	24	7.7	310	10	US-09-903-925-423	Sequence 423, App
44	24	7.7	310	10	US-09-906-760A-423	Sequence 423, App
45	24	7.7	310	10	US-09-903-823-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-10-410-842A-18
; Sequence 18, Application US/10410842A
; Publication No. US20030236396A1
; GENERAL INFORMATION:
; APPLICANT: Fasel et al
; TITLE OF INVENTION: SECRETORY SIGNAL SEQUENCES AND USES THEREOF
; FILE REFERENCE: 29964/37635A
; CURRENT APPLICATION NUMBER: US/10/410,842A
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/371,029
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-842A-18

Query Match 7.7%; Score 24; DB 15; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 2
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||

Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 3
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 4
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 5
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 6
US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 7
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-841-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 8
US-09-904-011-423
; Sequence 423, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 9
US-09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 10
US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 11
US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 12
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

```
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-942-423

  Query Match             7.7%;  Score 24;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 13
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,859
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-859-423

  Query Match             7.7%;  Score 24;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 14
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
```

```
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,204
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-204-423

  Query Match             7.7%;  Score 24;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 15
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Pong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,820
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
```

; ORGANISM: Homo Sapien
US-09-904-820-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190
```

Search completed: June 15, 2004, 11:14:52
Job time : 39 secs

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:06:35 ; Search time 14 Seconds
(without alignments)
2129.955 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHPFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	146	2	F70313	hypothetical prote
2	8	2.6	204	2	A89919	conserved hypothet
3	8	2.6	208	2	D83431	type III export pr
4	8	2.6	506	2	T02400	probable beta-gluc
5	8	2.6	959	2	E85276	hypothetical prote
6	7	2.3	118	1	G1YC	gene 1 protein - S
7	7	2.3	128	2	C83448	succinate dehydrog
8	7	2.3	137	2	B41047	exsB protein - Pse
9	7	2.3	137	2	E83433	exoenzyme S synthe
10	7	2.3	173	2	B90241	hypothetical prote
11	7	2.3	177	2	E85833	partial probable s
12	7	2.3	177	2	B90988	partial probable s
13	7	2.3	194	2	T28889	hypothetical prote
14	7	2.3	208	2	T03627	GTP-binding protei
15	7	2.3	208	2	T01588	GTP-binding protei
16	7	2.3	214	2	T47268	phosphatidylserine
17	7	2.3	224	2	D71915	hydrogenase, cytoc
18	7	2.3	232	2	S60984	hypothetical prote
19	7	2.3	246	2	F91238	PTS system, fructo
20	7	2.3	246	2	B86086	PTS system, fructo
21	7	2.3	249	2	G84224	hypothetical prote
22	7	2.3	255	2	B72474	hypothetical prote
23	7	2.3	267	2	B83705	phosphonates trans
24	7	2.3	269	1	C69651	prolipoprotein dia
25	7	2.3	280	2	H83623	probable chemotaxi
26	7	2.3	287	2	E75159	hypothetical prote
27	7	2.3	322	2	E69009	cation antiporter
28	7	2.3	324	2	T27302	hypothetical prote
29	7	2.3	332	1	DEBYG1	glyceraldehyde-3-p
30	7	2.3	332	1	DEBYG2	glyceraldehyde-3-p
31	7	2.3	332	2	C72485	probable high-affi
32	7	2.3	335	2	S29813	glyceraldehyde-3-p
33	7	2.3	337	2	AI2360	hypothetical prote
34	7	2.3	348	2	B84143	L-iditol 2-dehydro
35	7	2.3	359	2	H65201	pts system, fructo
36	7	2.3	380	2	H75159	3-isopropylmalate
37	7	2.3	387	2	B90533	nitrogen fixation
38	7	2.3	402	2	G83367	hypothetical prote
39	7	2.3	421	2	H86217	protein T27G7.16 [
40	7	2.3	422	2	D70110	aminotransferase (
41	7	2.3	429	2	AG2718	MFS permease [impo
42	7	2.3	429	2	C97500	hypothetical prote
43	7	2.3	445	2	S75859	hypothetical prote
44	7	2.3	452	2	A70389	L-seryl-tRNASec se
45	7	2.3	473	2	T28118	hypothetical prote

ALIGNMENTS

RESULT 1
F70313
hypothetical protein aq_142 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
C;Accession: F70313
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70313
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-146 <AQF>
A;Cross-references: GB:AE000675; NID:g2982863; PIDN:AAC06501.1; PID:g2982881; GB:AE0006
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_142
C;Superfamily: Aquifex aeolicus hypothetical protein aq_142

Query Match 2.6%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
||||||||
Db 5 VLIVLAVI 12

RESULT 2
A89919
conserved hypothetcial protein SA1250 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Jun-2003
C;Accession: A89919
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <KUR>
A;Cross-references: GB:BA000018; PID:g13701215; PIDN:BAB42510.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1250
C;Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain ho

```
  Query Match             2.6%;  Score 8;  DB 2;  Length 204;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IAGIIGGV 249
              ||||||||
Db        181 IAGIIGGV 188


RESULT 3
D83431
type III export protein PscK PA1724 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83431
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05113.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: pscK; PA1724

  Query Match             2.6%;  Score 8;  DB 2;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 SRRLRLRL 11
              ||||||||
Db        160 SRRLRLRL 167


RESULT 4
T02400
probable beta-glucosidase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02400; F84878
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
A;Reference number: Z14667
A;Accession: T02400
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-506 <ROU>
A;Cross-references: EMBL:AC004521; NID:g3128166; PIDN:AAC16091.1; PID:g3128187
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <STO>
A;Cross-references: GB:AE002093; NID:g3128187; PIDN:AAC16091.1; GSPDB:GN00139
C;Genetics:
A;Gene: F4I1.26; At2g44450
A;Map position: 2
A;Introns: 50/3; 74/1; 93/3; 119/1; 145/1; 174/2; 259/3; 370/1; 380/3; 415/1; 447/2
C;Superfamily: Agrobacterium beta-glucosidase

  Query Match             2.6%;  Score 8;  DB 2;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 LVVLIVLA 257
              ||||||||
Db          9 LVVLIVLA 16


RESULT 5
E85276
hypothetical protein AT4g24020 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: E85276
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spri
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-959 <STO>
A;Cross-references: GB:NC_001268; NID:g7269251; PIDN:CAB81320.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g24020
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

  Query Match             2.6%;  Score 8;  DB 2;  Length 959;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 EAVNLKSS 37
              ||||||||
Db        300 EAVNLKSS 307


RESULT 6
G1YC
gene 1 protein - Synechococcus sp. (strain PCC 6301)
C;Species: Synechococcus sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S10825
R;Cozens, A.L.; Walker, J.E.
J. Mol. Biol. 194, 359-383, 1987
A;Title: The organization and sequence of the genes for ATP synthase subunits in the cy
A;Reference number: S07286; MUID:87311713; PMID:3041005
A;Accession: S10825
A;Molecule type: DNA
A;Residues: 1-118 <COZ>
A;Cross-references: EMBL:X05302; NID:g48009; PIDN:CAA28922.1; PID:g48011
C;Superfamily: gene 1 protein
C;Keywords: membrane protein

  Query Match             2.3%;  Score 7;  DB 1;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        251 VVLIVLA 257
              |||||||
Db         75 VVLIVLA 81


RESULT 7
C83448
succinate dehydrogenase (C subunit) PA1581 [imported] - Pseudomonas aeruginosa (strain
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83448
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
```

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <STO>
A;Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AAG04970.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: sdhC; PA1581
C;Superfamily: succinate dehydrogenase 14K hydrophobic protein

Query Match 2.3%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VVLIVLA 257
|||||||
Db 117 VVLIVLA 123

RESULT 8
B41047
exsB protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 08-Oct-1999
C;Accession: B41047
R;Frank, D.W.; Iglewski, B.H.
J. Bacteriol. 173, 6460-6468, 1991
A;Title: Cloning and sequence analysis of a trans-regulatory locus required for exoenzym
A;Reference number: A41047; MUID:92011420; PMID:1655713
A;Accession: B41047
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <FRA>
A;Cross-references: GB:M64975; NID:g151217; PIDN:AAA25815.1; PID:g151219
C;Superfamily: Pseudomonas aeruginosa exsB protein

Query Match 2.3%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LRLRLYA 13
|||||||
Db 41 LRLRLYA 47

RESULT 9
E83433
exoenzyme S synthesis protein B PA1712 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83433
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <STO>
A;Cross-references: GB:AE004597; GB:AE004091; NID:g9947671; PIDN:AAG05101.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: exsB; PA1712
C;Superfamily: Pseudomonas aeruginosa exsB protein

Query Match 2.3%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LRLRLYA 13
|||||||
Db 41 LRLRLYA 47

RESULT 10
B90241
hypothetical protein SSO0903 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: B90241
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: GB:AE006641; NID:g13814083; PIDN:AAK41185.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO0903

Query Match 2.3%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 IIGGVLV 251
|||||||
Db 102 IIGGVLV 108

RESULT 11
E85833
partial probable sensor kinase Z3235 [imported] - Escherichia coli (strain O157:H7, sub
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85833
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85833
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <STO>
A;Cross-references: GB:AE005174; NID:g12516269; PIDN:AAG57129.1; GSPDB:GN00145; UWGP:Z3
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3235

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GGVLVVL 253
|||||||
Db 139 GGVLVVL 145

RESULT 12
B90988
partial probable sensor kinase ECs2874 [similarity] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C;Accession: B90988
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36297.1; PID:g13362343; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2874

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GGVLVVL 253
|||||||
Db 139 GGVLVVL 145

RESULT 13
T28889
hypothetical protein T14B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T28889
R;Pavello, T.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid T14B4.
A;Reference number: Z20539
A;Accession: T28889
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-194 <FAV>
A;Cross-references: EMBL:U50191; PIDN:AAA91238.1; CESP:T14B4.5
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T14B4.5
A;Introns: 49/2; 104/2; 137/3
C;Superfamily: Caenorhabditis elegans hypothetical protein T14B4.5

Query Match 2.3%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAV 258
|||||||
Db 93 VLIVLAV 99

RESULT 14
T03627
GTP-binding protein Rab6 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03627
R;Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995
A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana ta
A;Reference number: Z14896; MUID:95303981; PMID:7784525
A;Accession: T03627
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-208 <HAI>
A;Cross-references: EMBL:L29273; NID:g623585; PIDN:AAA74117.1; PID:g623586
A;Experimental source: strain SR1
C;Genetics:
A;Gene: Rab6
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;16-23/Region: nucleotide-binding motif A (P-loop)
F;122-125/Region: GTP-binding NKXD motif
F;152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
|||||||
Db 187 VNLKSSN 193

RESULT 15
T01588
GTP-binding protein At2g44610 - Arabidopsis thaliana
N;Alternate names: protein F16B22.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Mar-2001
C;Accession: T01588; F84880
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A;Reference number: Z14284
A;Accession: T01588
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <ROU>
A;Cross-references: EMBL:AC003672; NID:g3341671; PIDN:AAC27463.1; PID:g3341681
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE002093; NID:g3341681; PIDN:AAC27463.1; GSPDB:GN00139
C;Genetics:
A;Gene: F16B22.10; At2g44610
A;Map position: 2
A;Introns: 39/3; 63/2; 93/1; 130/2; 160/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;16-23/Region: nucleotide-binding motif A (P-loop)
F;122-125/Region: GTP-binding NKXD motif
F;152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
|||||||
Db 187 VNLKSSN 193

Search completed: June 15, 2004, 11:12:36
Job time : 15 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:10 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHPFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	146	1	Y142_AQUAE	O66537 aquifex aeo
2	7	2.3	118	1	ATPZ_SYNP6	P08443 synechococc
3	7	2.3	137	1	EXSB_PSEAE	P26994 pseudomonas
4	7	2.3	224	1	XLR1_MOUSE	Q9z114 mus musculu
5	7	2.3	232	1	YOZ1_YEAST	Q99210 saccharomyc
6	7	2.3	269	1	LGT_BACSU	O34752 bacillus su
7	7	2.3	280	1	CHR2_PSEAE	Q9i6v7 pseudomonas
8	7	2.3	331	1	G3P2_YEAST	P00358 saccharomyc
9	7	2.3	331	1	G3P3_YEAST	P00359 saccharomyc
10	7	2.3	335	1	G3P1_TRIKO	P17729 trichoderma
11	7	2.3	359	1	PTWC_ECOLI	P32672 escherichia
12	7	2.3	374	1	RL4_TRYBB	P49669 trypanosoma
13	7	2.3	380	1	LE22_PYRAB	Q9v1j0 pyrococcus
14	7	2.3	387	1	SRB2_HUMAN	Q9p1w8 homo sapien
15	7	2.3	422	1	CSD_BORBU	O51111 borrelia bu
16	7	2.3	452	1	SELA_AQUAE	O67140 aquifex aeo
17	7	2.3	473	1	YS81_CAEEL	Q09621 caenorhabdi
18	7	2.3	491	1	CPB4_RABIT	P00178 oryctolagus
19	7	2.3	491	1	CPB5_RABIT	P12789 oryctolagus
20	7	2.3	501	1	C6AH_DROME	Q9v770 drosophila
21	7	2.3	502	1	C6AN_DROME	Q9v771 drosophila
22	7	2.3	505	1	NDHF_BACSU	P39755 bacillus su
23	7	2.3	515	1	ROCA_OCEIH	Q8erf4 oceanobacil
24	7	2.3	515	1	SYM_BRUME	Q8yh17 brucella me
25	7	2.3	515	1	SYM_BRUSU	P59078 brucella su
26	7	2.3	574	1	IRL2_MOUSE	Q9ers7 mus musculu
27	7	2.3	578	1	OXAA_PSEAE	Q9ht06 pseudomonas
28	7	2.3	586	1	HOL1_YEAST	P53389 saccharomyc
29	7	2.3	697	1	CEAD_ECOLI	P17998 escherichia
30	7	2.3	758	1	SC18_YEAST	P18759 saccharomyc
31	7	2.3	774	1	VP4_ROTHT	P11200 human rotav
32	7	2.3	775	1	VP4_ROTHM	P11197 human rotav
33	7	2.3	776	1	VP4_ROTHN	P11199 human rotav
34	7	2.3	805	1	YC26_METJA	Q58623 methanococc
35	7	2.3	806	1	AD1B_MOUSE	Q8r534 mus musculu
36	7	2.3	810	1	SYFB_ANASP	Q8ymh5 anabaena sp
37	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
38	7	2.3	1105	1	YEGB_ECOLI	P38097 escherichia
39	7	2.3	1129	1	HPS5_HUMAN	Q9upz3 homo sapien
40	7	2.3	1234	1	YNX5_CAEEL	P34578 caenorhabdi
41	7	2.3	2871	1	FBN1_BOVIN	P98133 bos taurus
42	7	2.3	2871	1	FBN1_HUMAN	P35555 homo sapien
43	7	2.3	2871	1	FBN1_MOUSE	Q61554 mus musculu
44	7	2.3	2871	1	FBN1_PIG	Q9tv36 sus scrofa
45	7	2.3	3014	1	CLR1_HUMAN	Q9nyq6 homo sapien

ALIGNMENTS

RESULT 1
Y142_AQUAE
ID Y142_AQUAE STANDARD; PRT; 146 AA.
AC O66537;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_142.
GN AQ_142.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC ---

CC ---
DR EMBL; AE000675; AAC06501.1; -.
DR PIR; F70313; F70313.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 146 AA; 16321 MW; 9E98228A820CC2B2 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
||||||||
Db 5 VLIVLAVI 12

RESULT 2
ATPZ_SYNP6
ID ATPZ_SYNP6 STANDARD; PRT; 118 AA.
AC P08443;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein I.
GN ATPI.
OS Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.

```
OX   NCBI_TaxID=1139;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311713; PubMed=3041005;
RA   Cozens A.L., Walker J.E.;
RT   "The organization and sequence of the genes for ATP synthase subunits
RT   in the cyanobacterium Synechococcus 6301. Support for an
RT   endosymbiotic origin of chloroplasts.";
RL   J. Mol. Biol. 194:359-383(1987).
CC   -!- FUNCTION: A possible function for this protein is to guide the
CC       assembly of the membrane sector of the ATPase enzyme complex.
CC   -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X05302; CAA28922.1; -.
DR   PIR; S10825; G1YC.
KW   Hydrogen ion transport; CF(0); Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     73     93       POTENTIAL.
FT   TRANSMEM     94    114       POTENTIAL.
SQ   SEQUENCE   118 AA;  13455 MW;  16B76A47F76CC196 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         251 VVLIVLA 257
               |||||||
Db          75 VVLIVLA 81


RESULT 3
EXSB_PSEAE
ID   EXSB_PSEAE     STANDARD;      PRT;   137 AA.
AC   P26994;
DT   01-AUG-1992 (Rel. 23, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Exoenzyme S synthesis protein B.
GN   EXSB OR PA1712.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=92011420; PubMed=1655713;
RA   Frank D.W., Iglewski B.H.;
RT   "Cloning and sequence analysis of a trans-regulatory locus required
RT   for exoenzyme S synthesis in Pseudomonas aeruginosa.";
RL   J. Bacteriol. 173:6460-6468(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
CC   -!- SIMILARITY: TO Y.ENTEROCOLITICA VIRB.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M64975; AAA25815.1; -.
DR   EMBL; AE004597; AAG05101.1; -.
DR   PIR; B41047; B41047.
DR   PIR; E83433; E83433.
KW   Complete proteome.
FT   CONFLICT     62     62       R -> W (IN REF. 1).
SQ   SEQUENCE   137 AA;  14996 MW;  F7367E7AB301C4BA CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           7 LRLRLYA 13
               |||||||
Db          41 LRLRLYA 47


RESULT 4
XLR1_MOUSE
ID   XLR1_MOUSE     STANDARD;      PRT;   224 AA.
AC   Q9Z1L4;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Retinoschisin precursor (X-linked juvenile retinoschisis protein
DE   homolog).
GN   RS1 OR RS1H OR XLRS1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RX   MEDLINE=99160474; PubMed=10051329;
RA   Gehrig A.E., Warneke-Wittstock R., Sauer C.G., Weber B.H.F.;
RT   "Isolation and characterization of the murine X-linked juvenile
RT   retinoschisis (Rs1h) gene.";
RL   Mamm. Genome 10:303-307(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Brunner B., Todt T., Lenzner S., Stout K., Schulz U., Ropers H.-H.,
RA   Kalscheuer V.M.;
RT   "Genomic structure and comparative analysis of seven contiguous genes
RT   disclose a large region with conserved gene order in human Xp22.2-
RT   p22.1.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=99148018; PubMed=10023077;
RA   Reid S.N., Akhmedov N.B., Piriev N.I., Kozak C.A., Danciger M.,
RA   Farber D.B.;
RT   "The mouse X-linked juvenile retinoschisis cDNA: expression in
RT   photoreceptors.";
RL   Gene 227:257-266(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
```

```
RA   Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May be active in cell adhesion processes during retinal
CC       development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- TISSUE SPECIFICITY: Retinal specific.
CC   -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF084561; AAD21808.1; -.
DR   EMBL; AF084567; AAD21809.1; -.
DR   EMBL; AF084562; AAD21809.1; JOINED.
DR   EMBL; AF084563; AAD21809.1; JOINED.
DR   EMBL; AF084564; AAD21809.1; JOINED.
DR   EMBL; AF084565; AAD21809.1; JOINED.
DR   EMBL; AF084566; AAD21809.1; JOINED.
DR   EMBL; AJ011381; CAA09601.1; -.
DR   EMBL; BC046422; AAH46422.1; -.
DR   HSSP; P12259; 1CZT.
DR   MGD; MGI:1336189; Rs1h.
DR   InterPro; IPR000421; FA58_C.
DR   InterPro; IPR008979; Gal_bind_like.
DR   Pfam; PF00754; F5_F8_type_C; 1.
DR   SMART; SM00231; FA58C; 1.
DR   PROSITE; PS01285; FA58C_1; 1.
DR   PROSITE; PS01286; FA58C_2; FALSE_NEG.
DR   PROSITE; PS50022; FA58C_3; 1.
KW   Cell adhesion; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    224       RETINOSCHISIN.
FT   DOMAIN      63    219       F5/8 TYPE C.
FT   DISULFID    63    219       BY SIMILARITY.
SQ   SEQUENCE   224 AA;  25575 MW;  4536203CC00E90E4 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 FFLLLLF 24
              |||||||
Db          8 FFLLLLF 14


RESULT 5
YOZ1_YEAST
ID   YOZ1_YEAST     STANDARD;      PRT;   232 AA.
AC   Q99210;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein YOR111W.
GN   YOR111W OR YOR3237W OR O3237.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / FY1679;
RX   MEDLINE=97060020; PubMed=8904341;
RA   Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C.,
RA   Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.;
RT   "Sequencing and analysis of 51 kb on the right arm of chromosome XV
RT   from Saccharomyces cerevisiae reveals 30 open reading frames.";
RL   Yeast 12:281-288(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97344368; PubMed=9200815;
RA   Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA   Schwager C., Paces V., Sander C., Ansorge W.;
RT   "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
RL   Yeast 13:655-672(1997).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: Belongs to the maf family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X94335; CAA64031.1; -.
DR   EMBL; X90518; CAA62105.1; -.
DR   EMBL; Z75019; CAA99309.1; -.
DR   PIR; S60984; S60984.
DR   HSSP; Q02169; 1EX2.
DR   GermOnline; 143699; -.
DR   SGD; S0005637; YOR111W.
DR   InterPro; IPR003697; Maf.
DR   Pfam; PF02545; Maf; 1.
DR   TIGRFAMs; TIGR00172; maf; 1.
KW   Hypothetical protein.
FT   ACT_SITE     52     52       POTENTIAL.
SQ   SEQUENCE   232 AA;  26477 MW;  C0A83ED2AE20BE13 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 VYFDNKI 84
              |||||||
Db        166 VYFDNKI 172


RESULT 6
LGT_BACSU
ID   LGT_BACSU      STANDARD;      PRT;   269 AA.
AC   O34752;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-) (Spore
DE   germination protein gerP).
GN   LGT OR GERF OR BSU34990.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Robinson C., Rivolta C., Karamata D., Moir A.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RA   Lazarevic V., Soldo B., Rivolta C., Reynolds S., Mauel C.,
RA   Karamata D.;
RT   "Nucleotide sequence of the 300-304 chromosomal segment of Bacillus
RT   subtilis.";
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   -!- FUNCTION: Transfers the N-acyl diglyceride group on what will
CC       become the N-terminal cysteine of membrane lipoproteins.
CC   -!- PATHWAY: Lipoproteins biosynthesis; first step.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the lgt family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF017113; AAC67287.1; -.
DR   EMBL; Z99121; CAB15504.1; -.
DR   PIR; C69651; C69651.
DR   SubtiList; BG12611; lgt.
DR   InterPro; IPR001640; LGT.
DR   Pfam; PF01790; LGT; 1.
DR   ProDom; PD005412; LGT; 1.
DR   TIGRFAMs; TIGR00544; lgt; 1.
DR   PROSITE; PS01311; LGT; 1.
KW   Transferase; Transmembrane; Germination; Complete proteome.
FT   TRANSMEM     18     38       POTENTIAL.
FT   TRANSMEM     52     72       POTENTIAL.
FT   TRANSMEM     89    109       POTENTIAL.
FT   TRANSMEM    116    136       POTENTIAL.
FT   TRANSMEM    177    197       POTENTIAL.
FT   TRANSMEM    205    225       POTENTIAL.
FT   TRANSMEM    236    256       POTENTIAL.
SQ   SEQUENCE   269 AA;  30619 MW;  6D2E00DC07482C68 CRC64;
```

```
  Query Match             2.3%;  Score 7;  DB 1;  Length 269;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLIVLAV 258
              |||||||
Db        245 VLIVLAV 251


RESULT 7
CHR2_PSEAE
ID   CHR2_PSEAE     STANDARD;      PRT;   280 AA.
AC   Q9I6V7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Chemotaxis protein methyltransferase 2 (EC 2.1.1.80).
GN   CHER2 OR PA0175.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
CC   -!- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC       CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC       RESIDUES IN MCP (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC       = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC   -!- SIMILARITY: Contains 1 cheR-type methyltransferase domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE004455; AAG03565.1; -.
DR   PIR; H83623; H83623.
DR   HSSP; P07801; 1AF7.
DR   InterPro; IPR000780; CheR_Metranf.
DR   InterPro; IPR001601; Methyltransf.
DR   Pfam; PF01739; CheR; 1.
DR   Pfam; PF03705; CheR_N; 1.
DR   PRINTS; PR00996; CHERMTFRASE.
DR   SMART; SM00138; MeTrc; 1.
DR   PROSITE; PS50123; CHER; 1.
KW   Transferase; Methyltransferase; Complete proteome.
FT   DOMAIN       10    280       CHER-TYPE METHYLTRANSFERASE.
SQ   SEQUENCE   280 AA;  32028 MW;  FD2AF1491DDC57FB CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LSRRLRL 9
              |||||||
Db         49 LSRRLRL 55
```

```
RESULT 8
G3P2_YEAST
ID   G3P2_YEAST     STANDARD;      PRT;   331 AA.
AC   P00358;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Glyceraldehyde 3-phosphate dehydrogenase 2 (EC 1.2.1.12) (GAPDH 2).
GN   TDH2 OR GPD2 OR YJR009C OR J1433.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=92160396; PubMed=1789010;
RA   Mountain H.A., Korch C.;
RT   "TDH2 is linked to MET3 on chromosome X of Saccharomyces cerevisiae.";
RL   Yeast 7:873-880(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80137492; PubMed=6244283;
RA   Holland J.P., Holland M.J.;
RT   "Structural comparison of two nontandemly repeated yeast
RT   glyceraldehyde-3-phosphate dehydrogenase genes.";
RL   J. Biol. Chem. 255:2596-2605(1980).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / FY1679;
RA   de Haan M., Smits P.H.M., Grivell L.A.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 23-36; 71-76; 80-85; 198-212; 225-231 AND 321-330.
RC   STRAIN=ATCC 38531 / Y41;
RX   MEDLINE=95255188; PubMed=7737086;
RA   Norbeck J., Blomberg A.;
RT   "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
RT   resolved proteins from isogene families in Saccharomyces cerevisiae
RT   by microsequencing of in-gel trypsin generated peptides.";
RL   Electrophoresis 16:149-156(1995).
RN   [5]
RP   SEQUENCE OF 1-12.
RC   STRAIN=K12 / W3110;
RA   Frutiger S., Hughes G.J., Sanchez J.-C., Hochstrasser D.F.;
RL   Submitted (FEB-1996) to Swiss-Prot.
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC       NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC   -!- PATHWAY: Second phase of glycolysis; first step.
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: THERE ARE THREE GENES FOR G3PDH IN YEAST.
CC   -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC       dehydrogenase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60157; CAA42725.1; -.
DR   EMBL; V01301; CAA24608.1; ALT_SEQ.
DR   EMBL; X87611; CAA60931.1; -.
DR   EMBL; Z49509; CAA89531.1; -.
DR   PIR; S57024; DEBYG1.
DR   HSSP; P06977; 1GAD.
DR   GermOnline; 141845; -.
DR   SWISS-2DPAGE; P00358; YEAST.
DR   COMPLUYEAST-2DPAGE; P00358; -.
DR   SGD; S0003769; TDH2.
DR   GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
DR   GO; GO:0005811; C:lipid particle; IDA.
DR   GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IDA.
DR   InterPro; IPR000173; GAP_dhdrogenase.
DR   InterPro; IPR006424; GAPDH-I.
DR   Pfam; PF00044; gpdh; 1.
DR   Pfam; PF02800; gpdh_C; 1.
DR   PRINTS; PR00078; G3PDHDRGNASE.
DR   TIGRFAMs; TIGR01534; GAPDH-I; 1.
DR   PROSITE; PS00071; GAPDH; 1.
KW   Glycolysis; Oxidoreductase; NAD; Multigene family.
FT   INIT_MET      0      0
FT   BINDING     149    149       GLYCERALDEHYDE 3-PHOSPHATE.
FT   ACT_SITE    176    176       ACTIVATES THIOL GROUP DURING CATALYSIS.
FT   CONFLICT     76     76       E -> A (IN REF. 4).
SQ   SEQUENCE   331 AA;  35715 MW;  3998B6F655AFDFC4 CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 EVVALND 122
              |||||||
Db         26 EVVALND 32


RESULT 9
G3P3_YEAST
ID   G3P3_YEAST     STANDARD;      PRT;   331 AA.
AC   P00359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Glyceraldehyde 3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3).
GN   TDH3 OR GPD3 OR YGR192C OR G7576.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80027306; PubMed=385592;
RA   Holland J.P., Holland M.J.;
RT   "The primary structure of a glyceraldehyde-3-phosphate dehydrogenase
RT   gene from Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 254:9839-9845(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=95373283; PubMed=7645350;
RA   Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M.,
RA   Nombela C.;
RT   "The complete sequence of a 9037 bp DNA fragment of the right arm of
RT   Saccharomyces cerevisiae chromosome VII.";
RL   Yeast 11:587-591(1995).
RN   [3]
RP   SEQUENCE OF 46-57.
RC   STRAIN=S288c;
RX   MEDLINE=95203288; PubMed=7895733;
RA   Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA   Volpe T., Warner J.R., McLaughlin C.S.;
RT   "Protein identifications for a Saccharomyces cerevisiae protein
RT   database.";
RL   Electrophoresis 15:1466-1486(1994).
RN   [4]
RP   PARTIAL SEQUENCE.
RC   STRAIN=ATCC 38531 / Y41, and ATCC 44827 / SKQ2N;
RX   MEDLINE=95255188; PubMed=7737086;
RA   Norbeck J., Blomberg A.;
RT   "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
RT   resolved proteins from isogene families in Saccharomyces cerevisiae
RT   by microsequencing of in-gel trypsin generated peptides.";
```

```
RL   Electrophoresis 16:149-156(1995).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC       NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC   -!- PATHWAY: Second phase of glycolysis; first step.
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: THERE ARE THREE GENES FOR G3PDH IN YEAST.
CC   -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC       dehydrogenase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V01300; CAA24607.1; -.
DR   EMBL; J01324; AAA88714.1; -.
DR   EMBL; X82408; CAA57803.1; -.
DR   EMBL; Z72977; CAA97218.1; -.
DR   PIR; S55870; DEBYG2.
DR   HSSP; P06977; 1GAD.
DR   GermOnline; 141504; -.
DR   SWISS-2DPAGE; P00359; YEAST.
DR   COMPLUYEAST-2DPAGE; P00359; -.
DR   SGD; S0003424; TDH3.
DR   GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
DR   GO; GO:0005811; C:lipid particle; IDA.
DR   GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IDA.
DR   InterPro; IPR000173; GAP_dhdrogenase.
DR   InterPro; IPR006424; GAPDH-I.
DR   Pfam; PF00044; gpdh; 1.
DR   Pfam; PF02800; gpdh_C; 1.
DR   PRINTS; PR00078; G3PDHDRGNASE.
DR   TIGRFAMs; TIGR01534; GAPDH-I; 1.
DR   PROSITE; PS00071; GAPDH; 1.
KW   Glycolysis; Oxidoreductase; NAD; Multigene family.
FT   INIT_MET      0      0
FT   BINDING     149    149       GLYCERALDEHYDE 3-PHOSPHATE.
FT   ACT_SITE    176    176       ACTIVATES THIOL GROUP DURING CATALYSIS.
FT   CONFLICT    135    135       E -> V (IN REF. 1).
FT   CONFLICT    247    247       N -> D (IN REF. 1).
FT   CONFLICT    328    328       V -> I (IN REF. 1).
SQ   SEQUENCE   331 AA;  35615 MW;  CFFE94A335C648B5 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 EVVALND 122
              |||||||
Db         26 EVVALND 32


RESULT 10
G3P1_TRIKO
ID   G3P1_TRIKO     STANDARD;      PRT;   335 AA.
AC   P17729;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH1).
OS   Trichoderma koningii.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX   NCBI_TaxID=55202;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M3947;
RX   MEDLINE=93176825; PubMed=8439569;
RA   Watanabe H., Hasumi K., Fukushima Y., Sakai K., Endo A.;
RT   "Cloning of two isozymes of Trichoderma koningii glyceraldehyde-3-
RT   phosphate dehydrogenase with different sensitivity to koningic
RT   acid.";
RL   Biochim. Biophys. Acta 1172:43-48(1993).
RN   [2]
RP   SEQUENCE OF 1-31.
RC   STRAIN=M3947;
RX   MEDLINE=91031446; PubMed=2226438;
RA   Sakai K., Hasumi K., Endo A.;
RT   "Two glyceraldehyde-3-phosphate dehydrogenase isozymes from the
RT   koningic acid (heptelidic acid) producer Trichoderma koningii.";
RL   Eur. J. Biochem. 193:195-202(1990).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC       NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC   -!- ENZYME REGULATION: INHIBITED BY KONINGIC ACID THROUGH THE
CC       INTERACTION OF CYSTEINE RESIDUES WITH KONINGIC ACID EVEN AT VERY
CC       LOW CONCENTRATIONS.
CC   -!- PATHWAY: Second phase of glycolysis; first step.
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: THIS PROTEIN IS A KONINGIC ACID
CC       (ANTIBIOTIC)-RESISTANT GAPDH ISOZYME, EXPRESSED BY THE KONINGIC
CC       ACID PRODUCING TRICHODERMA KONINGII. IT IS PRESENT UNDER
CC       ANTIBIOTIC PRODUCTION.
CC   -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC       dehydrogenase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14519; BAA03392.1; -.
DR   PIR; S13205; S13205.
DR   HSSP; P56649; 1DSS.
DR   InterPro; IPR000173; GAP_dhdrogenase.
DR   InterPro; IPR006424; GAPDH-I.
DR   Pfam; PF00044; gpdh; 1.
DR   Pfam; PF02800; gpdh_C; 1.
DR   PRINTS; PR00078; G3PDHDRGNASE.
DR   TIGRFAMs; TIGR01534; GAPDH-I; 1.
DR   PROSITE; PS00071; GAPDH; 1.
KW   Glycolysis; Oxidoreductase; NAD; Multigene family.
FT   INIT_MET      0      0
FT   BINDING     149    149       GLYCERALDEHYDE 3-PHOSPHATE.
FT   ACT_SITE    176    176       ACTIVATES THIOL GROUP DURING CATALYSIS.
SQ   SEQUENCE   335 AA;  36121 MW;  D3F9A01754281A22 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 EVVALND 122
              |||||||
Db         27 EVVALND 33


RESULT 11
PTWC_ECOLI
ID   PTWC_ECOLI     STANDARD;      PRT;   359 AA.
AC   P32672;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   PTS system, fructose-like-2 IIC component (Phosphotransferase enzyme
DE   II, C component).
GN   FRWC OR B3949.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
```

```
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=94089392; PubMed=8265357;
RA   Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA   Daniels D.L.;
RT   "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT   region from 89.2 to 92.8 minutes.";
RL   Nucleic Acids Res. 21:5408-5417(1993).
RN   [2]
RP   DISCUSSION OF SEQUENCE.
RX   MEDLINE=95291446; PubMed=7773398;
RA   Reizer J., Reizer A., Saier M.H. Jr.;
RT   "Novel phosphotransferase system genes revealed by bacterial genome
RT   analysis -- a gene cluster encoding a unique Enzyme I and the proteins
RT   of a fructose-like permease system.";
RL   Microbiology 141:961-971(1995).
CC   -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
CC       sugar phosphotransferase system (PTS), a major carbohydrate active
CC       -transport system. The IICD domains contain the sugar binding site
CC       and the transmembrane channel; the IIA domain contains the primary
CC       phosphorylation site (the donor is phospho-HPr); IIA transfers its
CC       phosphoryl group to the IIB domain which finally transfers it to
CC       the sugar.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 PTS EIIC domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00006; AAC43055.1; -.
DR   EMBL; AE000469; AAC76931.1; -.
DR   PIR; H65201; H65201.
DR   EcoGene; EG11908; frwC.
DR   InterPro; IPR003352; Ptrans_EIIC.
DR   InterPro; IPR006327; PTS_IIC_fruct.
DR   Pfam; PF02378; PTS_EIIC; 1.
DR   TIGRFAMs; TIGR01427; PTS_IIC_fructo; 1.
KW   Phosphotransferase system; Sugar transport; Transmembrane;
KW   Inner membrane; Complete proteome.
FT   TRANSMEM     19     39       POTENTIAL.
FT   TRANSMEM     60     80       POTENTIAL.
FT   TRANSMEM     99    119       POTENTIAL.
FT   TRANSMEM    135    155       POTENTIAL.
FT   TRANSMEM    176    196       POTENTIAL.
FT   TRANSMEM    216    236       POTENTIAL.
FT   TRANSMEM    251    271       POTENTIAL.
FT   TRANSMEM    290    310       POTENTIAL.
FT   TRANSMEM    314    334       POTENTIAL.
SQ   SEQUENCE   359 AA;  37086 MW;  1CB60AF9FF6CCDAD CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 359;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IAGIIGG 248
              |||||||
Db        108 IAGIIGG 114


RESULT 12
RL4_TRYBB
ID   RL4_TRYBB      STANDARD;      PRT;   374 AA.
AC   P49669;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   60S ribosomal protein L4 (L1).
GN   RPL4 OR RPL1.
OS   Trypanosoma brucei brucei.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX   NCBI_TaxID=5702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=427;
RA   Wilson K., Uyetake L., Boothroyd J.C.;
RL   Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z54340; CAA91141.1; -.
DR   InterPro; IPR002136; Ribosomal_L4/L1E.
DR   Pfam; PF00573; Ribosomal_L4; 1.
DR   PROSITE; PS00939; RIBOSOMAL_L1E; 1.
KW   Ribosomal protein.
SQ   SEQUENCE   374 AA;  41886 MW;  67415135001F9804 CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 RRLRLRL 11
              |||||||
Db        323 RRLRLRL 329


RESULT 13
LE22_PYRAB
ID   LE22_PYRAB     STANDARD;      PRT;   380 AA.
AC   Q9V1J0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit 2 (EC 4.2.1.33)
DE   (Isopropylmalate isomerase 2) (Alpha-IPM isomerase 2) (IPMI 2).
GN   LEUC2 OR PYRAB04370 OR PAB0287.
OS   Pyrococcus abyssi.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=29292;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GE5 / Orsay;
RX   MEDLINE=22511545; PubMed=12622808;
RA   Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA   Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA   Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT   "An integrated analysis of the genome of the hyperthermophilic
RT   archaeon Pyrococcus abyssi.";
RL   Mol. Microbiol. 47:1495-1512(2003).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- COFACTOR: Binds 1 4Fe-4S cluster per subunit (By similarity).
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: Belongs to the aconitase/IPM isomerase family. LeuC 2
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

```
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AJ248284; CAB49359.1; -.
DR   PIR; H75159; H75159.
DR   HAMAP; MF_01027; -; 1.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR006251; Cis-H_aconitase.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR01343; hacA_fam; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL       262    262       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       320    320       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       323    323       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   380 AA;  41088 MW;  B22EE1E6D8016FAD CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 DEITIEL 133
              |||||||
Db        221 DEITIEL 227


RESULT 14
SRB2_HUMAN
ID   SRB2_HUMAN     STANDARD;      PRT;   387 AA.
AC   Q9P1W8; Q8WWA5; Q9NQK8;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Signal-regulatory protein beta-2 precursor (SIRP-beta-2) (SIRP-b2).
GN   SIRPB2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Placenta;
RX   MEDLINE=21036165; PubMed=11185750;
RA   Ichigotani Y., Matsuda S., Machida K., Oshima K., Iwamoto T.,
RA   Yamaki K., Hayakawa T., Hamaguchi M.;
RT   "Molecular cloning of a novel human gene (SIRP-B2) which encodes a new
RT   member of the SIRP/SHPS-1 protein family.";
RL   J. Hum. Genet. 45:378-382(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Probable immunoglobulin-like cell surface receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=Q9P1W8-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9P1W8-2; Sequence=VSP_007027;
CC         Note=No experimental confirmation available;
CC       Name=3;
CC         IsoId=Q9P1W8-3; Sequence=VSP_007028;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Detected in liver, and at very low levels in
CC       brain, heart, lung, pancreas, kidney, placenta and skeletal
CC       muscle.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AB042624; BAA95692.1; -.
DR   EMBL; AL138804; CAC00474.1; -.
DR   EMBL; BC020629; AAH20629.1; ALT_INIT.
DR   Genew; HGNC:15757; SIRPB2.
DR   MIM; 605466; -.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
```

```
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Repeat; Signal; Transmembrane; Immunoglobulin domain; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL       1     28       POTENTIAL.
FT   CHAIN       29    387       SIGNAL-REGULATORY PROTEIN BETA-2.
FT   DOMAIN      29    360       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   361    383       POTENTIAL.
FT   DOMAIN     384    387       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      29    137       IG-LIKE V-TYPE.
FT   DOMAIN     146    245       IG-LIKE C1-TYPE 1.
FT   DOMAIN     252    340       IG-LIKE C1-TYPE 2.
FT   DISULFID    53    119       POTENTIAL.
FT   DISULFID   168    226       POTENTIAL.
FT   DISULFID   271    329       POTENTIAL.
FT   CARBOHYD   243    243       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   268    268       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   309    309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   317    317       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     1     33       Missing (in isoform 2).
FT                               /FTId=VSP_007027.
FT   VARSPLIC   144    360       Missing (in isoform 3).
FT                               /FTId=VSP_007028.
FT   CONFLICT   263    263       A -> V (IN REF. 2).
FT   CONFLICT   286    286       L -> S (IN REF. 2).
SQ   SEQUENCE   387 AA;  42495 MW;  F7F20C9F86E0E64B CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        152 VGKTATL 158
              |||||||
Db         45 VGKTATL 51


RESULT 15
CSD_BORBU
ID   CSD_BORBU      STANDARD;      PRT;   422 AA.
AC   O51111;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable cysteine desulfurase (EC 4.4.1.-).
GN   CSD OR BB0084.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35210 / B31;
RX   MEDLINE=98065943; PubMed=9403685;
RA   Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA   Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA   Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA   Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA   van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA   Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA   Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA   Smith H.O., Venter J.C.;
RT   "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT   burgdorferi.";
RL   Nature 390:580-586(1997).
CC   -!- FUNCTION: Catalyzes the removal of elemental sulfur and selenium
CC       atoms from L-cysteine, L-cystine, L-selenocysteine, and L-
CC       selenocystine to produce L-alanine (By similarity).
CC   -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC   -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC       aminotransferases. Csd subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE001121; AAC66472.1; -.
DR   PIR; D70110; D70110.
DR   HSSP; P77444; 1JF9.
DR   TIGR; BB0084; -.
DR   InterPro; IPR000192; Aminotrans_V.
DR   Pfam; PF00266; aminotran_5; 1.
DR   PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW   Lyase; Pyridoxal phosphate; Complete proteome.
FT   BINDING     235    235       PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ   SEQUENCE   422 AA;  48124 MW;  0D37CE39059C2EDD CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 422;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 NIAGIIG 247
              |||||||
Db        292 NIAGIIG 298


Search completed: June 15, 2004, 11:10:30
Job time : 11 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:50 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	253	81.6	310	11	Q9EPK4	Q9epk4 mus musculu
2	245	79.0	310	11	Q9D1M9	Q9d1m9 mus musculu
3	152	49.0	310	11	Q9D8B7	Q9d8b7 mus musculu
4	64	20.6	64	11	Q8BT59	Q8bt59 mus musculu
5	24	7.7	309	4	Q96FL1	Q96fl1 homo sapien
6	24	7.7	310	4	Q9BX67	Q9bx67 homo sapien
7	24	7.7	355	4	Q8WWL8	Q8wwl8 homo sapien
8	8	2.6	92	2	Q8RQG2	Q8rqg2 bacillus ce
9	8	2.6	131	5	Q8I8S1	Q8i8s1 anopheles g
10	8	2.6	165	12	Q8AZH5	Q8azh5 rabbit hemo
11	8	2.6	204	16	Q99U70	Q99u70 staphylococ
12	8	2.6	204	16	Q8NWR5	Q8nwr5 staphylococ
13	8	2.6	204	16	Q8CSL1	Q8csl1 staphylococ
14	8	2.6	206	2	P95439	P95439 pseudomonas
15	8	2.6	208	16	Q9I313	Q9i313 pseudomonas
16	8	2.6	215	16	Q81R03	Q81r03 bacillus an
17	8	2.6	215	16	Q81DY6	Q81dy6 bacillus ce
18	8	2.6	246	5	Q9XY46	Q9xy46 ctenocephal
19	8	2.6	317	5	Q8I8D9	Q8i8d9 entamoeba h
20	8	2.6	324	16	Q8NLA6	Q8nla6 corynebacte
21	8	2.6	400	10	Q9LT44	Q9lt44 arabidopsis
22	8	2.6	443	16	Q7WIH9	Q7wih9 bordetella
23	8	2.6	443	16	Q7W6K5	Q7w6k5 bordetella
24	8	2.6	443	16	Q7VYK6	Q7vyk6 bordetella
25	8	2.6	462	16	Q8XKW0	Q8xkw0 clostridium
26	8	2.6	506	10	O64879	O64879 arabidopsis
27	8	2.6	959	10	O22987	O22987 arabidopsis
28	8	2.6	959	10	Q84TH9	Q84th9 arabidopsis
29	8	2.6	1005	5	Q8T7M0	Q8t7m0 bombyx mori
30	8	2.6	1065	16	Q81BF4	Q81bf4 bacillus ce
31	7	2.3	65	5	Q8IAB5	Q8iab5 caenorhabdi
32	7	2.3	67	4	Q8NI85	Q8ni85 homo sapien
33	7	2.3	68	2	Q8GAF5	Q8gaf5 arthrobacte
34	7	2.3	85	9	Q8SC57	Q8sc57 stx2 conver
35	7	2.3	85	9	Q7Y345	Q7y345 stx1 conver
36	7	2.3	85	9	Q7Y2N4	Q7y2n4 stx2 conver
37	7	2.3	85	12	Q99GX8	Q99gx8 helicoverpa
38	7	2.3	92	10	Q8LFP4	Q8lfp4 arabidopsis
39	7	2.3	92	10	Q8GXY9	Q8gxy9 arabidopsis
40	7	2.3	95	10	Q9FE08	Q9fe08 perilla fru
41	7	2.3	115	12	Q7TFD7	Q7tfd7 rhesus cyto
42	7	2.3	121	2	Q93HQ4	Q93hq4 streptococc
43	7	2.3	126	16	Q89H27	Q89h27 bradyrhizob
44	7	2.3	128	16	Q9I3D7	Q9i3d7 pseudomonas
45	7	2.3	133	16	Q83AG2	Q83ag2 coxiella bu

ALIGNMENTS

RESULT 1
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

```
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   EMBL; BC024357; AAH24357.1; -.
DR   EMBL; AK032833; BAC28049.1; -.
DR   MGD; MGI:1933825; Jam3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;

  Query Match             81.6%;  Score 253;  DB 11;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1e-264;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEV 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEV 117

Qy        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177

Qy        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297

Qy        298 EEGDFRHKSSFVI 310
              |||||||||||||
Db        298 EEGDFRHKSSFVI 310


RESULT 2
Q9D1M9
ID   Q9D1M9      PRELIMINARY;      PRT;   310 AA.
AC   Q9D1M9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003326; BAB22715.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34819 MW;  6692BCAD68EA4B1D CRC64;

  Query Match             79.0%;  Score 245;  DB 11;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-256;
  Matches  245;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEV 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEV 117

Qy        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177

Qy        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297

Qy        298 EEGDF 302
              |||||
Db        298 EEGDF 302


RESULT 3
Q9D8B7
ID   Q9D8B7      PRELIMINARY;      PRT;   310 AA.
AC   Q9D8B7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=21085660; PubMed=11217851;
```

```
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK008187; BAB25519.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34855 MW;  C74884EABE234680 CRC64;

  Query Match             49.0%;  Score 152;  DB 11;  Length 310;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-155;
  Matches  252;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117

Qy        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYNWYRND 177

Qy        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297

Qy        298 EEGDFRHKSSFVI 310
              |||||||||||||
Db        298 EEGDFRHKSSFVI 310


RESULT 4
Q8BT59
ID   Q8BT59      PRELIMINARY;      PRT;    64 AA.
AC   Q8BT59;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Junction cell adhesion molecule 3 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK017692; BAC25526.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   64 AA;  6996 MW;  AF46BC30AA6D0C11 CRC64;

  Query Match             20.6%;  Score 64;  DB 11;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-61;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        247 GGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKS 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKS 60

Qy        307 SFVI 310
              ||||
Db         61 SFVI 64


RESULT 5
Q96FL1
ID   Q96FL1      PRELIMINARY;      PRT;   309 AA.
AC   Q96FL1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010690; AAH10690.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
FT   NON_TER       1      1
SQ   SEQUENCE   309 AA;  34917 MW;  50C5B1B7872E8DF3 CRC64;

  Query Match              7.7%;  Score 24;  DB 4;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-17;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        166 PRPHYSWYRNDVPLPTDSRANPRF 189


RESULT 6
Q9BX67
ID   Q9BX67      PRELIMINARY;      PRT;   310 AA.
AC   Q9BX67;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule 3 precursor (Junctional adhesion
DE   molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE   FLJ90288) (Hypothetical protein FLJ90828).
GN   JAM-2 OR JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
```

```
RA   Cunningham S.A., Arrate M.P., Tran T.M.;
RT   "Cloning of Human Junctional Adhesion Molecule 3.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT   "Heterogeneity of endothelial junctions is reflected by differential
RT   expression and specific subcellular localization of the three JAM
RT   family members.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT   "Junctional adhesion molecules (JAMs) and interendothelial
RT   junctions.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT   "Characterization of Junctional Adhesional Molecule-3 on Human
RT   Platelets: A New Member of Immunoglobulin Superfamily.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   EMBL; AF448478; AAM20925.1; -.
DR   EMBL; AK074769; BAC11195.1; -.
DR   EMBL; AK075309; BAC11538.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Signal.
FT   SIGNAL        1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;

  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-17;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT 7
Q8WWL8
ID   Q8WWL8      PRELIMINARY;      PRT;   355 AA.
AC   Q8WWL8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule 3.
GN   JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hearn T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Phillips H.M.;
RT   "Narrowing the critical region within 11q24-qter for hypoplastic left
RT   heart and identification of a candidate gene, JAM3, expressed during
RT   cardiogenesis.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416101; CAC94776.1; -.
DR   Genew; HGNC:15532; JAM3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   CHAIN         76    355       JUNCTION ADHESION MOLECULE 3.
SQ   SEQUENCE   355 AA;  39602 MW;  8B1577DEA7B1D4F8 CRC64;

  Query Match             7.7%;  Score 24;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 PRPHYSWYRNDVPLPTDSRANPRF 190
              ||||||||||||||||||||||||
Db        212 PRPHYSWYRNDVPLPTDSRANPRF 235


RESULT 8
Q8RQG2
ID   Q8RQG2      PRELIMINARY;      PRT;    92 AA.
AC   Q8RQG2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Probable NAD(P)H-flavin oxidoreductase (Fragment).
GN   CMK16.
OS   Bacillus cereus.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1396;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tim-r01;
RA   Nishizawa M., Itoi Y., Ito S., Inoue M.;
RT   "Genes induced by glycine in Bacillus cereus.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB083554; BAB88982.1; -.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000415; Nitroreductase.
DR   Pfam; PF00881; Nitroreductase; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   92 AA;  10168 MW;  B9C9B25BAF889B39 CRC64;

  Query Match             2.6%;  Score 8;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        123 RKEVDEIT 130
              ||||||||
Db         81 RKEVDEIT 88


RESULT 9
Q8I8S1
ID   Q8I8S1      PRELIMINARY;      PRT;   131 AA.
AC   Q8I8S1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Odorant-binding protein G.38B.a.
OS   Anopheles gambiae (African malaria mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=7165;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Xu P., Smith D.P.;
```

```
RT   "Identification of distinct families of odorant-binding in the genome
RT   of Anopheles gambiae.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY146730; AAO12090.1; -.
DR   GO; GO:0005549; F:odorant binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR006170; PBP_GOBP.
DR   Pfam; PF01395; PBP_GOBP; 1.
SQ   SEQUENCE   131 AA;  14884 MW;  FC7D52E9740E2A64 CRC64;

  Query Match             2.6%;  Score 8;  DB 5;  Length 131;
  Best Local Similarity   100.0%;  Pred. No. 5.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        246 IGGVLVVL 253
              ||||||||
Db          7 IGGVLVVL 14


RESULT 10
Q8AZH5
ID   Q8AZH5      PRELIMINARY;      PRT;   165 AA.
AC   Q8AZH5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Capsid protein (Fragment).
GN   VP60.
OS   Rabbit hemorrhagic disease virus (RHDV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC   Lagovirus.
OX   NCBI_TaxID=11976;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=94-02;
RX   MEDLINE=22422426; PubMed=12536296;
RA   Le Gall-Recule G., Zwingelstein F., Laurent S., de Boisseson C.,
RA   Portejoie Y., Rasschaert D.;
RT   "Phylogenetic analysis of rabbit haemorrhagic disease virus in France
RT   between 1993 and 2000, and the characterisation of RHDV antigenic
RT   variants.";
RL   Arch. Virol. 148:65-81(2003).
DR   EMBL; AJ535102; CAD59257.1; -.
DR   InterPro; IPR004005; Calici_coat.
DR   Pfam; PF00915; Calici_coat; 1.
FT   NON_TER       1      1
FT   NON_TER     165    165
SQ   SEQUENCE   165 AA;  16991 MW;  9A6E06A848F69ED8 CRC64;

  Query Match             2.6%;  Score 8;  DB 12;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 PAAVPVGK 154
              ||||||||
Db         54 PAAVPVGK 61


RESULT 11
Q99U70
ID   Q99U70      PRELIMINARY;      PRT;   204 AA.
AC   Q99U70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Conserved hypothetcial protein (Hypothetical protein SAV1417).
GN   SAV1417 OR SA1250.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=158878, 158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003362; BAB57579.1; -.
DR   EMBL; AP003133; BAB42510.1; -.
DR   PIR; A89919; A89919.
DR   InterPro; IPR008934; AcPase_VanPerase.
DR   InterPro; IPR000326; PA_PTPase.
DR   Pfam; PF01569; PAP2; 1.
DR   SMART; SM00014; acidPPc; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   204 AA;  22685 MW;  009CF65D8B1PBDF2 CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 204;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IAGIIGGV 249
              ||||||||
Db        181 IAGIIGGV 188


RESULT 12
Q8NWR5
ID   Q8NWR5      PRELIMINARY;      PRT;   204 AA.
AC   Q8NWR5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Conserved hypothetcial protein.
GN   MW1306.
OS   Staphylococcus aureus (strain MW2).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=196620;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22040717; PubMed=12044378;
RA   Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA   Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA   Yamamoto K., Hiramatsu K.;
RT   "Genome and virulence determinants of high virulence community-
RT   acquired MRSA.";
RL   Lancet 359:1819-1827(2002).
DR   EMBL; AP004826; BAB95171.1; -.
DR   InterPro; IPR008934; AcPase_VanPerase.
DR   InterPro; IPR000326; PA_PTPase.
DR   Pfam; PF01569; PAP2; 1.
KW   Complete proteome.
SQ   SEQUENCE   204 AA;  22715 MW;  0CFDFB30PB03C497 CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 204;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IAGIIGGV 249
              ||||||||
Db        181 IAGIIGGV 188


RESULT 13
Q8CSL1
ID   Q8CSL1      PRELIMINARY;      PRT;   204 AA.
AC   Q8CSL1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
```

```
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Conserved hypothetical protein.
GN   SE1109.
OS   Staphylococcus epidermidis.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1282;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 12228;
RA   Zhang Y., Ren S., Li H., Pu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA   Chen Z., Wen Y.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE016747; AAO04706.1; -.
DR   InterPro; IPR008934; AcPase_VanPerase.
DR   InterPro; IPR000326; PA_PTPase.
DR   Pfam; PF01569; PAP2; 1.
DR   SMART; SM00014; acidPPc; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   204 AA;  22838 MW;  CC6635270009F674 CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 204;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IAGIIGGV 249
              ||||||||
Db        181 IAGIIGGV 188


RESULT 14
P95439
ID   P95439      PRELIMINARY;      PRT;   206 AA.
AC   P95439;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   PscK.
GN   PSCK.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=388;
RX   MEDLINE=97126825; PubMed=8971719;
RA   Yahr T.L., Goranson J., Frank D.W.;
RT   "Exoenzyme S of Pseudomonas aeruginosa is secreted by a type III
RT   pathway.";
RL   Mol. Microbiol. 22:991-1003(1996).
DR   EMBL; U56077; AAC44782.1; -.
SQ   SEQUENCE   206 AA;  23971 MW;  8DD0E751E26BDFA8 CRC64;

  Query Match             2.6%;  Score 8;  DB 2;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 SRRLRLRL 11
              ||||||||
Db        160 SRRLRLRL 167


RESULT 15
Q9I313
ID   Q9I313      PRELIMINARY;      PRT;   208 AA.
AC   Q9I313;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Type III export protein PscK.
GN   PSCK OR PA1724.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004598; AAG05113.1; -.
DR   PIR; D83431; D83431.
KW   Complete proteome.
SQ   SEQUENCE   208 AA;  23898 MW;  74F6B5848FE9E5BE CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 8.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 SRRLRLRL 11
              ||||||||
Db        160 SRRLRLRL 167


Search completed: June 15, 2004, 11:11:55
Job time : 37 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:50:54 ; Search time 51.5 Seconds
(without alignments)
1700.771 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1633	100.0	310	3	AAB27278	Aab27278 Murine co
2	1633	100.0	310	3	AAB27272	Aab27272 Human con
3	1409	86.3	310	3	AAY96735	Aay96735 PRO1868,
4	1409	86.3	310	3	AAB33457	Aab33457 Human PRO
5	1409	86.3	310	3	AAB27276	Aab27276 Human con
6	1409	86.3	310	4	AAB80272	Aab80272 Human PRO
7	1409	86.3	310	4	AAM93905	Aam93905 Human pol
8	1409	86.3	310	4	AAM93323	Aam93323 Human pol
9	1409	86.3	310	4	AAU12440	Aau12440 Human PRO
10	1409	86.3	310	4	AAB80383	Aab80383 Secreted
11	1409	86.3	310	4	AAB80408	Aab80408 Secreted
12	1409	86.3	310	4	AAB80409	Aab80409 Secreted
13	1409	86.3	310	5	ABG92709	Abg92709 Human sec
14	1409	86.3	310	5	ABG91361	Abg91361 Novel hum
15	1409	86.3	310	5	ABB84947	Abb84947 Human PRO
16	1409	86.3	310	5	ABG65297	Abg65297 Human alb
17	1409	86.3	310	5	ABG65296	Abg65296 Human alb
18	1409	86.3	310	5	ABG65298	Abg65298 Human alb
19	1409	86.3	310	5	ABG31401	Abg31401 Human PRO
20	1409	86.3	310	5	ABB95553	Abb95553 Human ang
21	1409	86.3	310	6	ABU71650	Abu71650 Human PRO
22	1409	86.3	310	6	ABU72377	Abu72377 Novel hum
23	1409	86.3	310	6	ABU80867	Abu80867 Human sec
24	1409	86.3	310	6	ABO17884	Abo17884 Novel hum
25	1409	86.3	310	6	ABU71505	Abu71505 Human PRO
26	1409	86.3	310	6	ADA57610	Ada57610 Human sec
27	1409	86.3	310	6	ADA57611	Ada57611 Human sec
28	1409	86.3	310	6	ADA57309	Ada57309 Human sec
29	1409	86.3	310	6	ABP71277	Abp71277 Human jun
30	1409	86.3	310	6	ABU81138	Abu81138 Human PRO
31	1409	86.3	310	6	ABU71951	Abu71951 Human sec
32	1409	86.3	310	6	ABO01834	Abo01834 Novel hum
33	1409	86.3	310	6	ABU66838	Abu66838 Human PRO
34	1409	86.3	310	6	ABU54407	Abu54407 Human sec
35	1409	86.3	310	6	ABO47422	Abo47422 Human sec
36	1409	86.3	310	6	ABG73314	Abg73314 Human PRO
37	1409	86.3	310	6	ABU59919	Abu59919 Novel sec
38	1409	86.3	310	6	ABO25109	Abo25109 Human sec
39	1409	86.3	310	6	ABU64559	Abu64559 Human sec
40	1409	86.3	310	6	ABU67405	Abu67405 Human sec
41	1409	86.3	310	6	ABO14925	Abo14925 Human sec
42	1409	86.3	310	6	ABU60813	Abu60813 Human sec
43	1409	86.3	310	6	ABU67114	Abu67114 Human sec
44	1409	86.3	310	6	ABU81236	Abu81236 Human PRO
45	1409	86.3	310	6	ABU69682	Abu69682 Novel hum

ALIGNMENTS

RESULT 1
AAB27278
ID AAB27278 standard; protein; 310 AA.
XX
AC AAB27278;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine confluency regulated adhesion molecule 1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; mouse;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Mus sp.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA97189.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Example; Fig 8; 59pp; English.
XX
CC The present sequence is the murine confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1633; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;

```
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
AAB27272
ID   AAB27272 standard; protein; 310 AA.
XX
AC   AAB27272;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Human confluency regulated adhesion molecule 1 #1.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP002219.
XX
PR   11-MAR-1999;   99EP-00200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability.
XX
PS   Claim 1; Fig 3; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1633;  DB 3;  Length 310;

  Best Local Similarity   100.0%;  Pred. No. 1.2e-122;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 3
AAY96735
ID   AAY96735 standard; protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .30
FT                   /label= Signal_peptide
FT   Modified-site   26. .31
FT                   /note= "N-myristoylation site"
FT   Modified-site   69. .77
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   104. .107
FT                   /note= "N-glycosylation site"
FT   Modified-site   106. .109
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   107. .110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   192. .195
FT                   /note= "N-glycosylation site"
FT   Modified-site   215. .220
FT                   /note= "N-myristoylation site"
FT   Modified-site   226. .231
FT                   /note= "N-myristoylation site"
FT   Domain          243. .263
FT                   /label= Transmembrane_domain
FT   Modified-site   243. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   244. .249
FT                   /note= "N-myristoylation site"
FT   Modified-site   262. .267
FT                   /note= "N-myristoylation site"
FT   Modified-site   296. .299
FT                   /note= "Casein kinase II phosphorylation site"
```

XX
PN WO200036102-A2.
XX
PD 22-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US028634.
XX
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2000-431586/37.
DR N-PSDB; AAA51265.
XX
PT Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT transmembrane polypeptide.
XX
PS Claim 1; Fig 14; 154pp; English.
XX
CC This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC cancer-associated marker. The invention concerns novel secreted and
CC transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC sequences are useful in the recombinant production of PRO polypeptides,
CC as a hybridization probe to screen libraries to isolate cDNAs with
CC sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC used to produce transgenic animals useful for the development and
CC screening of therapeutically useful reagents. They can also be used in
CC gene therapy, e.g. to replace a defective gene
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 3; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||||:| |||||||||  ||| ||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
AAB33457
ID AAB33457 standard; protein; 310 AA.
XX
AC AAB33457;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.

```
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58622.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS   Claim 33; Fig 88; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central and
CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 3;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 5
AAB27276
ID   AAB27276 standard; protein; 310 AA.
XX
AC   AAB27276;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Human confluency regulated adhesion molecule 1 #2.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP002219.
XX
PR   11-MAR-1999;   99EP-00200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
DR   N-PSDB; AAA95306.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability.
XX
PS   Claim 2; Fig 6; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 3;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
AAB80272
ID   AAB80272 standard; protein; 310 AA.
XX
```

```
AC   AAB80272;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human PRO1868 protein.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
PF   22-FEB-2000; 2000WO-US004414.
XX
PR   07-JUL-1999;   99US-0143048P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N;
PI   Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ,  Kljavin IJ;
PI   Mather JP,  Pan J,  Paoni NF,  Roy MA,  Stewart TA,  Tumas D;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-081051/09.
DR   N-PSDB; AAF72433.
XX
PT   Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT   treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT   cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT   disease).
XX
PS   Claim 1; Fig 124; 393pp; English.
XX
CC   The present sequence is one of sixty one novel secreted and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful for treating skin
CC   diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC   gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC   diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC   cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC   ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC   disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC   infertility, AIDS and diabetes and retinal disorders such as retinitis
CC   pigmentosum. The PRO nucleic acids have applications in molecular
CC   biology, including use as hybridization probes, and in chromosome and
CC   gene mapping
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;

  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| |||||||||  ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
AAM93905
ID   AAM93905 standard; protein; 310 AA.
XX
AC   AAM93905;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 4051.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94867.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
```

```
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFPLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 8
AAM93323
ID   AAM93323 standard; protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94243.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFPLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 9
AAU12440
ID   AAU12440 standard; protein; 310 AA.
XX
AC   AAU12440;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO1868 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
```

PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21512.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 538; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||:| |||||||||  ||| ||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||  |||||:|||||||||||||  ::  |||||:||||||  |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:|||  |||  ||||||||||:| ||||||  |||  ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:||||:|||||||||  ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||  ||||||||||  |||:||:|||||||||  ||:=|||||||:|||  |||||||  |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 10
AAB80383
ID AAB80383 standard; protein; 310 AA.
XX
AC AAB80383;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #13.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 538-539; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations

XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 11
AAB80408
ID AAB80408 standard; protein; 310 AA.
XX
AC AAB80408;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #38.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 559-560; 601pp; English.
XX

```
CC   The present invention relates to 29 human secreted proteins. The
CC   invention is used to prevent autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. Also used in food
CC   preparations
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| ||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
ABG92709
ID   ABG92709 standard; protein; 310 AA.
XX
AC   ABG92709;
XX
DT   18-NOV-2002  (first entry)
XX
DE   Human secreted protein PRO1868.
XX
KW   Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW   PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW   inflammatory disorder; immune related disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW   autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW   psoriasis; allergic disease of the lung; graft-versus host disease;
KW   tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002098506-A1.
XX
PD   25-JUL-2002.
XX
PF   27-DEC-2001; 2001US-00033301.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-690475/74.
DR   N-PSDB; ABS68392.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides useful
PT   for diagnosis and treatment of inflammatory disorders and immune-related
PT   diseases, and identifying modulators.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to an isolated polypeptide having at least 80%
CC   amino acid sequence identity to secreted and transmembrane polypeptides
CC   PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC   PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC   cells and antibodies against PRO polypeptides. PRO proteins are useful
CC   for identifying modulators of the polypeptide. PRO1868 useful for the
CC   diagnosis and treatment of inflammatory and immune related diseases
CC   including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC   sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC   infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC   versus host disease and tumours. Pro nucleic acids are useful for
CC   constructing hybridisation probes for mapping the gene that encodes that
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   and for generating transgenic animals which are useful in the development
CC   and screening of therapeutically useful reagents. PRO nucleic acids are
CC   also useful for gene therapy, chromosome identification, and tissue
CC   typing. PRO proteins are useful as molecular weight markers for protein
CC   electrophoresis purposes. The anti-PRO antibodies are useful in
CC   diagnostic assays for PRO, e.g. detecting its expression in specific
CC   cells, tissues or serum and for affinity purification of PRO. The present
CC   sequence represents a PRO protein
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 5;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| ||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
```

```
Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 14
ABG91361
ID   ABG91361 standard; protein; 310 AA.
XX
AC   ABG91361;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Novel human secreted protein #7.
XX
KW   Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW   immunogenic.
XX
OS   Homo sapiens.
XX
PN   US2002098505-A1.
XX
PD   25-JUL-2002.
XX
PF   28-DEC-2001; 2001US-00033246.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-665999/71.
DR   N-PSDB; ABS67460.
XX
PT   New human secreted and transmembrane (PRO) polypeptides, useful for
PT   treating conditions requiring PRO polypeptides, for screening PRO
PT   antagonists and agonists useful as drug candidates.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to new human secreted and transmembrane proteins
CC   (PRO) and nucleic acids of the invention. The polypeptides can be
CC   administered therapeutically, especially by expressing encoding
CC   polynucleotides, e.g. in therapeutic compositions. They can be used to
CC   screen for PRO polypeptide antagonists and agonists useful to identify
CC   drug candidates. They can also be used to produce antibodies, useful to
CC   detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC   therapeutically (e.g. as antagonists or to target and/or deliver
CC   cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC   produce antisense sequences to inhibit polypeptide production. They can
CC   be used to produce probes and primers useful to detect or isolate
CC   sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC   sequences from other species. They are also useful for gene mapping and
CC   to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC   amino acid sequences of the invention
XX
SQ   Sequence 310 AA;

  Query Match             86.3%;  Score 1409;  DB 5;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-104;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| |||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
ABB84947
ID   ABB84947 standard; protein; 310 AA.
XX
AC   ABB84947;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO1868 protein sequence SEQ ID NO:262.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
```

PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88202.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 262; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 5; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  ||||  |||| ||||||||||:| |||||||||  ||| ||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||  |||||:|||||||||||||  ::  |||||:||||||  |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:|||  |||  ||||||||||:|  ||||||  |||  |||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:||||||:|||||||||  ||||||||||||||||||||:||||  |:|||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||  ||||||||||  |||:||:|||||||||  ||::||||||||:|||  ||||||||  |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

Search completed: June 15, 2004, 11:03:06
Job time : 52.5 secs

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1409	86.3	310	4	US-09-907-794A-423	Sequence 423, App
2	1409	86.3	310	4	US-09-905-125A-423	Sequence 423, App
3	1409	86.3	310	4	US-09-902-775A-423	Sequence 423, App
4	498	30.5	298	4	US-09-152-060-76	Sequence 76, Appl
5	478	29.3	312	4	US-09-254-465A-9	Sequence 9, Appli
6	478	29.3	312	4	US-09-907-794A-64	Sequence 64, Appl
7	478	29.3	312	4	US-09-905-125A-64	Sequence 64, Appl
8	478	29.3	312	4	US-09-902-775A-64	Sequence 64, Appl
9	449.5	27.5	300	4	US-09-254-465A-10	Sequence 10, Appl
10	415	25.4	299	3	US-09-188-930-331	Sequence 331, App
11	415	25.4	299	4	US-09-462-270-2	Sequence 2, Appli
12	415	25.4	299	4	US-09-254-465A-1	Sequence 1, Appli
13	415	25.4	299	4	US-09-312-283C-189	Sequence 189, App
14	415	25.4	299	4	US-09-312-283C-331	Sequence 331, App
15	415	25.4	299	4	US-09-907-794A-119	Sequence 119, App
16	415	25.4	299	4	US-09-905-125A-119	Sequence 119, App
17	415	25.4	299	4	US-09-902-775A-119	Sequence 119, App
18	403	24.7	299	3	US-09-188-930-189	Sequence 189, App
19	381.5	23.4	260	4	US-09-254-465A-23	Sequence 23, Appl
20	381.5	23.4	263	4	US-09-254-465A-25	Sequence 25, Appl
21	283	17.3	205	4	US-09-462-270-4	Sequence 4, Appli
22	242.5	14.8	319	1	US-08-597-495B-22	Sequence 22, Appl
23	242.5	14.8	319	3	US-09-068-051A-22	Sequence 22, Appl
24	242.5	14.8	319	4	US-09-336-536-67	Sequence 67, Appl
25	242.5	14.8	319	4	US-09-254-465A-6	Sequence 6, Appli
26	240.5	14.7	318	3	US-09-068-051A-32	Sequence 32, Appl
27	236.5	14.5	270	4	US-09-254-465A-24	Sequence 24, Appl
28	236.5	14.5	273	4	US-09-254-465A-26	Sequence 26, Appl
29	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
30	173.5	10.6	365	3	US-08-928-383B-2	Sequence 2, Appli
31	172.5	10.6	365	2	US-08-979-424-3	Sequence 3, Appli
32	172.5	10.6	365	3	US-09-272-496-2	Sequence 2, Appli
33	172.5	10.6	370	4	US-09-336-536-28	Sequence 28, Appl
34	171.5	10.5	341	4	US-09-336-536-29	Sequence 29, Appl
35	171.5	10.5	390	2	US-08-979-424-1	Sequence 1, Appli
36	171.5	10.5	390	4	US-09-907-794A-39	Sequence 39, Appl
37	171.5	10.5	390	4	US-09-905-125A-39	Sequence 39, Appl
38	171.5	10.5	390	4	US-09-902-775A-39	Sequence 39, Appl
39	167.5	10.3	365	4	US-09-336-536-40	Sequence 40, Appl
40	167.5	10.3	394	4	US-09-336-536-39	Sequence 39, Appl
41	166	10.2	1101	3	US-08-986-485-2	Sequence 2, Appli
42	163	10.0	313	4	US-09-700-397-4	Sequence 4, Appli
43	163	10.0	344	4	US-09-700-397-3	Sequence 3, Appli
44	161.5	9.9	246	4	US-09-336-536-31	Sequence 31, Appl
45	160	9.8	869	1	US-08-374-834-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

```
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-794A-423

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-133;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-125A-423

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 1.1e-133;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
```

```
Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:||||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 3
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Pilvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-775A-423

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-133;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:||||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970

```
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/068,368
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 298
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (42)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (58)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

  Query Match            30.5%;  Score 498;  DB 4;  Length 298;
  Best Local Similarity  37.0%;  Pred. No. 6.2e-42;
  Matches  117;  Conservative   61;  Mismatches  112;  Indels   26;  Gaps    9;

Qy          3 LSRRLRLRLYARLPHFFLLLLFRGCMI-----EAVNLKSSNRNPVVH--EFESVELSCII 55
              ::|| | ||         |||| |  ::     :|    :     ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRC 115
              |  :|   |:||||:     ::||:   :|||   | ::    ::|| ||||||:  |||
Db         52 TPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYI 294
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |  ||:      |  | :  :
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE-----TSFQKSNSSSKA 282

Qy        295 RTSEEGDFRHKSSFVI 310
              |  | ||:|  ||:|
Db        283 TTMSENDFKHTKSFII 298


RESULT 5
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 9
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-254-465A-9

  Query Match            29.3%;  Score 478;  DB 4;  Length 312;
  Best Local Similarity  36.3%;  Pred. No. 6.9e-40;
  Matches  110;  Conservative   62;  Mismatches  109;  Indels   22;  Gaps    8;

Qy          3 LSRRLRLRLYARLPHFFLLLLFRGCMI-----EAVNLKSSNRNPVVH--EFESVELSCII 55
              ::|| | ||         |||| |  ::     :|    :     ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRC 115
              |  :|   |:||||:     ::||:   :|||   | ::    ::|| ||||||:  |||
Db         52 TPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCF---ISSKQDGESYKSPGKHDGV 291
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |    | ::   | |:    : |
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENV 289

Qy        292 NYI 294
              ::
Db        290 QWL 292


RESULT 6
US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
```

```
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-64

  Query Match             29.3%;  Score 478;  DB 4;  Length 312;
  Best Local Similarity   36.3%;  Pred. No. 6.9e-40;
  Matches  110;  Conservative   62;  Mismatches  109;  Indels   22;  Gaps    8;

Qy          3 LSRRLRLRLYARLPHPFLLLLFRGCMI-----EAVNLKSSNRNPVVH--EFESVELSCII 55
              ::|| | ||         |||| |  ::     :|     :      ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRC 115
              |  :|   |:||||:     ::||:   :|||    | ::    ::|| ||||||:  |||
Db         52 TPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCP---ISSKQDGESYKSPGKHDGV 291
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |    | ::   | |:    : |
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENV 289

Qy        292 NYI 294
               ::
Db        290 QWL 292


RESULT 7
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-905-125A-64

  Query Match             29.3%;  Score 478;  DB 4;  Length 312;
```

```
  Best Local Similarity   36.3%;  Pred. No. 6.9e-40;
  Matches  110;  Conservative   62;  Mismatches  109;  Indels   22;  Gaps    8;

Qy          3 LSRRLRLRLYARLPHPFPLLLLFRGCMI-----EAVNLKSSNRNPVVH--EPESVELSCII 55
              ::|| | ||         |||| |  ::     :|    :     ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRC 115
              |  :|   |:||||:     ::||:   :|||   | ::    ::|| ||||||:  |||
Db         52 TPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRPQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCP---ISSKQDGESYKSPGKHDGV 291
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |    | ::   | |:    : |
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENV 289

Qy        292 NYI 294
               ::
Db        290 QWL 292


RESULT 8
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-775A-64

  Query Match             29.3%;  Score 478;  DB 4;  Length 312;
  Best Local Similarity   36.3%;  Pred. No. 6.9e-40;
  Matches  110;  Conservative   62;  Mismatches  109;  Indels   22;  Gaps    8;

Qy          3 LSRRLRLRLYARLPHPFPLLLLFRGCMI-----EAVNLKSSNRNPVVH--EPESVELSCII 55
              ::|| | ||         |||| |  ::     :|    :     ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRC 115
              |  :|   |:||||:     ::||:   :|||   | ::    ::|| ||||||:  |||
Db         52 TPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRPQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCP---ISSKQDGESYKSPGKHDGV 291
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |    | ::   | |:    : |
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENV 289

Qy        292 NYI 294
               ::
Db        290 QWL 292


RESULT 9
US-09-254-465A-10
; Sequence 10, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
```

```
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 10
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-254-465A-10

  Query Match           27.5%;  Score 449.5;  DB 4;  Length 300;
  Best Local Similarity   34.2%;  Pred. No. 4.8e-37;
  Matches  102;  Conservative   64;  Mismatches  117;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCMIEAV-----NLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQ 74
                ||  ||    :: ::      :: ::  :  | | ||::|:|  |:|  | ||:||| :|
Db         11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELI 134
                |  | ::::|    | |   |  : :   :||| |:  | | :|:    :   |::| |
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT-DSRANPRFQNS 193
                | | |   :|::| :|  | | | | :| |   |||::: : : | |::    | ||
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
                || :: ::| |:|: |   |||:||| | |  | | | |   |:  :||: ||:  |||
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
                ||:| ::  |:  || || | ::|:      :|||    :   |  ||:|:  |||::
Db        247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 10
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Human
US-09-188-930-331

  Query Match           25.4%;  Score 415;  DB 3;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
                | | :|     : :| : ||     : |   |:|||   :|  | ||:|||  |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
                | ::|||      |   |  | :   :||| |:  | | :|:         |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
                |  |   ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
                |  || |||: :   |:|:| | | |  |          ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
                ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 11
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
;  APPLICANT:  SmithKline Beecham Corporation
;  TITLE OF INVENTION:  Human P11 Antigen: A Cell Surface
;  TITLE OF INVENTION:  Receptor  Involved in Platelet Aggregation
;  FILE REFERENCE:  GH-70150US
;  CURRENT APPLICATION NUMBER: US/09/462,270
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/052,186
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-462-270-2

  Query Match           25.4%;  Score 415;  DB 4;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
                | | :|     : :| : ||     : |   |:|||   :|  | ||:|||  |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
                | ::|||      |   |  | :   :||| |:  | | :|:         |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
                |  |   ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
                |  || |||: :   |:|:| | | |  |          ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
                ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
```

```
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 1
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-254-465A-1

  Query Match             25.4%;  Score 415;  DB 4;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 PFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
              | | :|     : :| : ||     : |   |:|||   :|  | ||:||| |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
              | ::|||      |   | | :   :||| |:  | | :|:         |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
              |   |  ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
              |  || |||: :   |:|:| | | |  |           ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
              ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 13
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-189

  Query Match             25.4%;  Score 415;  DB 4;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 PFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
              | | :|     : :| : ||     : |   |:|||   :|  | ||:||| |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
              | ::|||      |   | | :   :||| |:  | | :|:         |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
              |   |  ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
              |  || |||: :   |:|:| | | |  |           ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
              ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 14
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-331

  Query Match             25.4%;  Score 415;  DB 4;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 PFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
              | | :|     : :| : ||     : |   |:|||   :|  | ||:||| |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
              | ::|||      |   | | :   :||| |:  | | :|:         |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
              |   |  ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
              |  || |||: :   |:|:| | | |  |           ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
              ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
```

```
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299

RESULT 15
US-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-119

  Query Match            25.4%;  Score 415;  DB 4;  Length 299;
  Best Local Similarity  33.8%;  Pred. No. 1.4e-33;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
              | | :|     : :| : ||     : |   |:|||   :|  | ||:|||  |   |
Db         15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
              | ::|||       |   |  | :   :||| |:  | | :|:        |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
              |  |   ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
              |  || |||: :   |:|:| | | |  |           ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
               ::  ||  || || |  :|:   | |         | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


Search completed: June 15, 2004, 11:06:31
Job time : 17.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:14 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1409	86.3	310	9	US-09-909-320-423	Sequence 423, App
2	1409	86.3	310	9	US-09-909-088B-423	Sequence 423, App
3	1409	86.3	310	9	US-09-905-291A-423	Sequence 423, App
4	1409	86.3	310	9	US-09-902-853-423	Sequence 423, App
5	1409	86.3	310	9	US-09-907-824-423	Sequence 423, App
6	1409	86.3	310	9	US-09-907-841-423	Sequence 423, App
7	1409	86.3	310	10	US-09-904-011-423	Sequence 423, App
8	1409	86.3	310	10	US-09-906-742-423	Sequence 423, App
9	1409	86.3	310	10	US-09-906-838-423	Sequence 423, App
10	1409	86.3	310	10	US-09-907-613-423	Sequence 423, App
11	1409	86.3	310	10	US-09-907-942-423	Sequence 423, App
12	1409	86.3	310	10	US-09-904-859-423	Sequence 423, App
13	1409	86.3	310	10	US-09-909-204-423	Sequence 423, App
14	1409	86.3	310	10	US-09-904-820-423	Sequence 423, App
15	1409	86.3	310	10	US-09-904-786-423	Sequence 423, App
16	1409	86.3	310	10	US-09-906-646-423	Sequence 423, App
17	1409	86.3	310	10	US-09-906-700-423	Sequence 423, App
18	1409	86.3	310	10	US-09-903-786-423	Sequence 423, App
19	1409	86.3	310	10	US-09-902-903-423	Sequence 423, App
20	1409	86.3	310	10	US-09-903-749A-423	Sequence 423, App
21	1409	86.3	310	10	US-09-904-119-423	Sequence 423, App
22	1409	86.3	310	10	US-09-904-956-423	Sequence 423, App
23	1409	86.3	310	10	US-09-902-736-423	Sequence 423, App
24	1409	86.3	310	10	US-09-907-794-423	Sequence 423, App
25	1409	86.3	310	10	US-09-903-943-423	Sequence 423, App
26	1409	86.3	310	10	US-09-904-462-423	Sequence 423, App
27	1409	86.3	310	10	US-09-907-925-423	Sequence 423, App
28	1409	86.3	310	10	US-09-902-692-423	Sequence 423, App
29	1409	86.3	310	10	US-09-903-520-423	Sequence 423, App
30	1409	86.3	310	10	US-09-905-056-423	Sequence 423, App
31	1409	86.3	310	10	US-09-909-064-423	Sequence 423, App
32	1409	86.3	310	10	US-09-904-553-423	Sequence 423, App
33	1409	86.3	310	10	US-09-905-381-423	Sequence 423, App
34	1409	86.3	310	10	US-09-905-088-423	Sequence 423, App
35	1409	86.3	310	10	US-09-907-575-423	Sequence 423, App
36	1409	86.3	310	10	US-09-905-075-423	Sequence 423, App
37	1409	86.3	310	10	US-09-902-759-423	Sequence 423, App
38	1409	86.3	310	10	US-09-902-634-423	Sequence 423, App
39	1409	86.3	310	10	US-09-902-713-423	Sequence 423, App
40	1409	86.3	310	10	US-09-907-979-423	Sequence 423, App
41	1409	86.3	310	10	US-09-902-615-423	Sequence 423, App
42	1409	86.3	310	10	US-09-903-925-423	Sequence 423, App
43	1409	86.3	310	10	US-09-906-760A-423	Sequence 423, App
44	1409	86.3	310	10	US-09-903-823-423	Sequence 423, App
45	1409	86.3	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

```
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-320-423

  Query Match           86.3%;  Score 1409;  DB 9;  Length 310;
  Best Local Similarity  85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| |||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              :  || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,088B
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-088B-423

  Query Match           86.3%;  Score 1409;  DB 9;  Length 310;
  Best Local Similarity  85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;
```

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  ||||  ||||  ||||||||||:|  |||||||||  |||  ||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 3
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423

Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  ||||  ||||  ||||||||||:|  |||||||||  |||  ||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

```
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,853
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: US/09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-853-423

  Query Match             86.3%;  Score 1409;  DB 9;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFPLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYSKPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 5
US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,824
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
```

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFPLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| ||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-841-423

Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFPLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| ||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| ||||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011

; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien

US-09-904-011-423

Query Match 86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||||:| |||||||||  |||  |||||||||||||  |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||  |||||:|||||||||||| ::  |||||:|||||  |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| |||  ||||||||||:|  ||||||  |||  ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||  ||||||||||||||||||||:||||  |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || ||||||||||  |||:||:|||||||||  ||::|||||||:|||  ||||||||  |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 8
US-09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

```
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-742-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |:|||:||| ||| |||||||||||:| |||||| ||| |||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||||| ||::|||||||:||| ||||||||  |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 9
US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Pong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,838
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-838-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;
```

```
Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| ||||:||:||||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 10
US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,613
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-613-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHPFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| ||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| ||||:||:||||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 11
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              |||  |  |||| |||| |||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVC.IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||| :| |||||| ||| ||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCNVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              |||||||||:|||||:||||||| | ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

```
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-859-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:|||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,204
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-204-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| |||||||| ||| ||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:|||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 14
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-423

Query Match 86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| ||||||||||:| |||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||:| |||||| ||| ||||||:|||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 15
US-09-904-786-423
; Sequence 423, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

```
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,786
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-786-423

  Query Match             86.3%;  Score 1409;  DB 10;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 3.6e-118;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||||:| |||||||||| ||| ||||||||||||| |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: June 15, 2004, 11:08:01
Job time : 39 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:59:09 ; Search time 14.5 Seconds
(without alignments)
2056.508 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	415	25.4	299	2	S56749	junctional adhesio
2	181	11.1	725	2	JE0099	neural cell adhesi
3	180	11.0	1088	1	IJXLNL	neural cell adhesi
4	178	10.9	1051	2	A39712	kinase-like protei
5	177	10.8	333	2	A31923	amalgam protein pr
6	172.5	10.6	858	1	IJRTNC	neural cell adhesi
7	169.5	10.4	725	1	IJMSNG	neural cell adhesi
8	169.5	10.4	1115	1	IJMSNL	neural cell adhesi
9	169	10.3	725	2	JE0100	neural cell adhesi
10	169	10.3	1092	1	JN0635	neural cell adhesi
11	167.5	10.3	3707	2	S18252	heparan sulfate pr
12	167.5	10.3	6642	2	T29757	protein UNC-89 - C
13	166	10.2	483	2	T17346	hypothetical prote
14	164.5	10.1	352	2	T33433	hypothetical prote
15	164.5	10.1	853	1	IJBONC	neural cell adhesi
16	164	10.0	7962	2	I38346	elastic titin - hu
17	163	10.0	761	1	IJHUNG	neural cell adhesi
18	162	9.9	5175	2	T20992	hypothetical prote
19	162	9.9	5198	2	T43290	hemicentin precurs
20	160	9.8	875	2	T33434	hypothetical prote
21	159.5	9.8	1277	2	T30532	neural cell adhesi
22	158.5	9.7	365	2	JC7780	coxsackie- and ade
23	157	9.6	1091	1	IJCHNL	neural cell adhesi
24	156	9.6	344	2	I56551	neurotrimin - rat
25	156	9.6	1323	2	PN0568	connectin 3B - chi
26	156	9.6	4162	2	T42633	connectin/titin -
27	154.5	9.5	272	2	I48268	biliary glycoprote
28	153.5	9.4	1033	2	S19247	cell adhesion prot
29	153	9.4	1273	2	T42405	sax-3 protein - Ca
30	152	9.3	538	2	JC2457	vascular cell adhe
31	151.5	9.3	811	2	A41054	fasciclin II, tran
32	151.5	9.3	873	2	B41054	fasciclin II PI-li
33	151.5	9.3	1427	2	I51669	tumor suppressor -
34	151	9.2	1091	2	A58532	glial cell membran
35	151	9.2	1894	2	C54689	protein-tyrosine-p
36	151	9.2	1912	2	A56178	protein-tyrosine-p
37	150	9.2	423	2	T29549	hypothetical prote
38	150	9.2	584	2	T08678	hypothetical prote
39	150	9.2	1694	2	S50065	sialoadhesin - mou
40	149.5	9.2	4391	2	A38096	perlecan precursor
41	149	9.1	1612	2	T30805	dutt1 protein - mo
42	148.5	9.1	871	1	I48696	protein-tyrosine k
43	148.5	9.1	881	1	I48697	protein-tyrosine k
44	148.5	9.1	1070	2	JC4593	protein-tyrosine k
45	148	9.1	947	1	B44294	unc-5 protein, lon

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'P',125-130;'FDKDXTIYLNXY';'LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 25.4%; Score 415; DB 2; Length 299;
Best Local Similarity 33.8%; Pred. No. 2.7e-26;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

```
Qy      18 PFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
           | | :|     : :| : ||     : |   |:|||   :|  | ||:|||  |   |
Db      15 PILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy      78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
           | ::|||       |   | | :   :||| |:  | | :|:         |: ::||| |
Db      73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy     138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
           |  |   ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db     131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy     198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
           |  || |||: :   |:|:| | | |  |          ||  : |:  |:  ||| ||:|
Db     191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy     257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
           ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
```

```
Db        251 GILVPGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 2
JE0099
neural cell adhesion molecule 1 - African clawed frog
N;Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match             11.1%;  Score 181;  DB 2;  Length 725;
  Best Local Similarity   28.8%;  Pred. No. 7.8e-07;
  Matches   60;  Conservative   33;  Mismatches   81;  Indels   34;  Gaps   11;

Qy         32 VNLK-----SSNRNPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
              ||||     :    |   ||:  | : ||    :| |  | |: | :|     | |   :
Db        107 VNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                  |  |      |:|  : ::|   ||||  ::|   | |::   |::|| | |
Db        162 ------RFVVLANNYLQIRGIKKTDEGTYRCEGRILA---RGEINYKDIQVIVNVPPTIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
               |: |   : ::  | | :::|:| |  || :   |:           :  ||  | :
Db        213 ARQLRVNATAKMAESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :  : | |||  :| |||:| || |
Db        264 QSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 3
IJXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LD
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pre
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             11.0%;  Score 180;  DB 1;  Length 1088;
  Best Local Similarity   28.8%;  Pred. No. 1.5e-06;
  Matches   60;  Conservative   33;  Mismatches   81;  Indels   34;  Gaps   11;

Qy         32 VNLK-----SSNRNPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
              ||||     :    |   ||:  | : ||    :| |  | |: | :|     | |   :
Db        107 VNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                  |  |      |:|  : ::|   ||||  ::|   | |::   |::|| | |
Db        162 ------RFVVLANNYLQIRGIKKTDEGTYRCEGRILA---RGEINYKDIQVIVNVPPTIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
               |: |   : ::  | | :::|:| |  || :   |:           :  ||  | :
Db        213 ARQLRVNATANMAESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :  : | |||  :| |||:| || |
Db        264 QSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 4
A39712
kinase-like protein klg precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C;Accession: A39712
R;Chou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A;Title: Characterization of a member of the immunoglobulin gene superfamily that possi
A;Reference number: A39712; MUID:91271300; PMID:1711213
A;Accession: A39712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1051 <CHO>
A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C;Keywords: ATP
F;775-1046/Domain: protein kinase homology <KIN>
F;783-791/Region: protein kinase ATP-binding motif

  Query Match             10.9%;  Score 178;  DB 2;  Length 1051;
  Best Local Similarity   28.3%;  Pred. No. 2.1e-06;
  Matches   72;  Conservative   29;  Mismatches  109;  Indels   44;  Gaps   12;

Qy         45 EP-ESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIW 103
              || : | :||  |  :   | |:| |  ||        : :   :: |  :      |
Db        496 EPNKEVTVSCSATGRE--KPTIQWTK-TDG--------SSLPSHVSHRAGI-----LSFH 539

Qy        104 NVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQES 163
              |:||||  | |  :| | :     |::|:| |      :   |  |  || |||  :
Db        540 KVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVYVTPKLEPEPTTVYQGHTAMFQCQ-A 596

Qy        164 EGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASN 223
              || | ||  |   |  |   |:  || |           |:||   |  :|||:| ||| |
Db        597 EGDPVPHIQWKGKDKIL-DPSKLLPRIQ------IMPNGSLVIYDVTTEDSGKYTCIAGN 649

Qy        224 DA--------------GAARCEGQDMEV-YD-LNIAGIIGGVLVVLIVLAVITMGICCA 266
                             |  ||      |  :   |:  |  |  |:: :  |  |
Db        650 SCNIKHREAFLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIIIVLGLMFYCKK 709
```

```
Qy        267 YRRGCFISSKQDGE 280
              |:   :    :||
Db        710 RRKAKRLKKHPEGE 723


RESULT 5
A31923
amalgam protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from Dr
A;Reference number: A31923; MUID:89028670; PMID:3141062
A;Accession: A31923
A;Molecule type: DNA
A;Residues: 1-333 <SEE>
A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C;Genetics:
A;Gene: FlyBase:Ama
A;Cross-references: FlyBase:FBgn0000071

  Query Match             10.8%;  Score 177;  DB 2;  Length 333;
  Best Local Similarity   27.2%;  Pred. No. 6.7e-07;
  Matches   53;  Conservative   38;  Mismatches   82;  Indels   22;  Gaps    6;

Qy         35 KSSNRNPVVHEPESVELSCIITHSQ-TSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTD 93
              ::: :: :| | :::||:|   |:     | | | :  :               :
Db        143 ENTPKSTLVTEGQNLELTC---HANGFPKPTISWAREHNAV------------MPAGGH 186

Qy         94 VFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVG 153
              :  : ::||| :| | |   | |  :| |   : |: | : |: :|   | |   | |
Db        187 LLAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVS 244

Qy        154 KTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDD 213
             :| |:|   :||| |   |::| |||   |  :    |::   : |  |  ::| ::|
Db        245 HSAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEED 301

Qy        214 SGQYYCIASNDAGAA 228
              | ||| |:|  | |
Db        302 FGDYYCNATNKLGHA 316


RESULT 6
IJRTNC
neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence for a
A;Reference number: S00846; MUID:88059265; PMID:3680385
A;Accession: S00846
A;Molecule type: mRNA
A;Residues: 1-858 <SMA>
A;Cross-references: EMBL:X06564
R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-364 <RES>
A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <M
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMM4>
F;430-492/Domain: immunoglobulin homology <IMM5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TMM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.6%;  Score 172.5;  DB 1;  Length 858;
  Best Local Similarity   27.1%;  Pred. No. 4.7e-06;
  Matches   61;  Conservative   43;  Mismatches   84;  Indels   37;  Gaps   13;

Qy         26 GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
              |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db        103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy         79 YFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
              |  :: |:  |  |     |:|  : ::|  ||||  ::|   | |::   |::||
Db        157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy        137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
              | |      :  : |   :|:: || | :::|:| |   || ::  |:  :       ::
Db        210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE------EDDE 262

Qy        195 FHV-NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
              |: : ::  |    | |:|  :| ||| | ||      ||  ::
Db        263 KHIFSDDSSELTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302


RESULT 7
IJMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N;Alternate names: NCAM-120
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00382; A44290
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonte
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-725 <BAR>
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00382
A;Molecule type: DNA
A;Residues: 642-656,'D',658-725 <BA2>
A;Cross-references: EMBL:X07195
R;Rougon, G.; Marshak, D.R.
```

J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 701/1
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 169.5; DB 1; Length 725;
Best Local Similarity 27.7%; Pred. No. 6.8e-06;
Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;

```
Qy          26 GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
               |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db         103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy          79 YFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
                 :: |:  |  |      |:|  : ::|   ||||  ::|   | |::   |::||
Db         157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy         137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
               | |     :  : |   :|:: || | :::|:|  |  || ::  |:  :   : | ::|
Db         210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-DERSRSSV 267

Qy         195 FHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                 |::  :    | |:|  :| ||| | ||      ||  ::
Db         268 ----SDSSEVTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302
```

RESULT 8
IJMSNL
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00844; S00384; A28281; A44290; S00383
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,'L'
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
A;Reference number: S00844; MUID:88067687; PMID:3684567
A;Accession: S00844
A;Molecule type: mRNA
A;Residues: 529-809,1077-1115 <SAN>
A;Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
R;Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJM
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status exper
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #st
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TMM>
F;730-1115/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 169.5; DB 1; Length 1115;
Best Local Similarity 27.7%; Pred. No. 1.1e-05;
Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;

```
Qy          26 GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
               |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db         103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy          79 YFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
                 :: |:  |  |      |:|  : ::|   ||||  ::|   | |::   |::||
Db         157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy         137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
               | |     :  : |   :|:: || | :::|:|  |  || ::  |:  :   : | ::|
Db         210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-DERSRSSV 267

Qy         195 FHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                 |::  :    | |:|  :| ||| | ||      ||  ::
Db         268 ----SDSSEVTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302
```

RESULT 9
JE0100

neural cell adhesion molecule 2 - African clawed frog
N;Alternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0100
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0100
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BAA25932.1; PID:g3116229
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.3%; Score 169; DB 2; Length 725;
Best Local Similarity 28.4%; Pred. No. 7.4e-06;
Matches 59; Conservative 33; Mismatches 82; Indels 34; Gaps 11;

```
Qy         32 VNLKSSNR-----NPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
              ||||    :       |   ||    | : ||     :| |  | |: | :|       | |    :
Db        107 VNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                  |  |      |:|  : ::|   ||||  ::|   | |::   |::|| | |:
Db        162 ------RFVVLANNYLQIRGIKKTDEGNYRCEGRILA---RGEINYKDIQVIVNVPPLIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
                |: |   : ::   | | :::|:| |  || :   |:          :  ||  | :
Db        213 ARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :    | |:|  :| |||:| || |
Db        264 KSEMTIYRVEKEDEAEYSCIANNQAGEA 291
```

RESULT 10
JN0635
neural cell adhesion molecule 2 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C;Accession: JN0635
R;Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993
A;Title: Two neural-cell adhesion molecule(NCAM)-encoding genes in Xenopus laevis are ex
A;Reference number: JN0635; MUID:93273239; PMID:7684721
A;Accession: JN0635
A;Molecule type: mRNA
A;Residues: 1-1092 <TON>
A;Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Genetics:
A;Gene: NCAM2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;317-381/Domain: immunoglobulin homology <IMM3>
F;413-475/Domain: immunoglobulin homology <IMM4>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;619-680/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1092/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.3%; Score 169; DB 1; Length 1092;
Best Local Similarity 28.4%; Pred. No. 1.2e-05;
Matches 59; Conservative 33; Mismatches 82; Indels 34; Gaps 11;

```
Qy         32 VNLKSSNR-----NPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
              ||||    :       |   ||    | : ||     :| |  | |: | :|       | |    :
Db        107 VNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                  |  |      |:|  : ::|   ||||  ::|   | |::   |::|| | |:
Db        162 ------RFVVLANNYLQIRGIKKTDEGNYRCEGRILA---RGEINYKDIQVIVNVPPLIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
                |: |   : ::   | | :::|:| |  || :   |:          :  ||  | :
Db        213 ARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :    | |:|  :| |||:| || |
Db        264 KSEMTIYRVEKEDEAEYSCIANNQAGEA 291
```

RESULT 11
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Pulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Has
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membr
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glo
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G rep
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicte

```
  Query Match             10.3%;  Score 167.5;  DB 2;  Length 3707;
  Best Local Similarity   26.2%;  Pred. No. 6.6e-05;
  Matches   55;  Conservative   26;  Mismatches   68;  Indels   61;  Gaps    9;

Qy         32 VNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKK---------IQDGQTTYVYFDN 82
Db       2812 INVRTSVHSVVVG--HSVEFECLALGD--PKPQVTWSKVGGHLRPGIVQSG--------- 2858

Qy         83 KIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKP--- 139
Db       2859 --------------TIIRIAHVELADAGQYRC---AATNAAGTTQSHVLLLVQALPQIS 2900

Qy        140 VTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNS 199
Db       2901 TPPEIRVPA----GSAAVFPCMAS-GYPTPAITWSKVDGDLPPDSRL------------- 2942

Qy        200 ETGTLVFNAVHKDDSGQYYCIASNDAGAAR 229
Db       2943 ENNMLMLPSVRPEDAGTYVCTATNRQGKVK 2972


RESULT 12
T29757
protein UNC-89 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C;Accession: T29757
R;Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid C09D1.
A;Reference number: Z20679
A;Accession: T29757
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6642 <DUZ>
A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
A;Experimental source: strain Bristol N2; clone C09D1
C;Genetics:
A;Gene: CESP:unc-89
A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; 6
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

  Query Match             10.3%;  Score 167.5;  DB 2;  Length 6642;
  Best Local Similarity   27.1%;  Pred. No. 0.00013;
  Matches   57;  Conservative   30;  Mismatches   68;  Indels   55;  Gaps    9;

Qy         45 EFESVELSCIITHSQTS----------DPRIEWKKIQDGQ----TTYVYFDNKIQGDLAG 90
Db       3828 EFVELLRSCTVTEKQQAILKCKVKGEPRPKIKWTK--EGKEVEMSARVRAEHKDDGTL-- 3883

Qy         91 RTDVFGKTSLRIWNVTRSDSAIYRCE--------------VVALNDRKEVDEITIELIVQ 136
Db       3884 --------TLTFDNVTQADAGEYRCEAENEYGSAWTEGPIIVTLEGAPKIDGEAPDFLQP 3935

Qy        137 VKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFH 196
Db       3936 VK--------PAVVTVGETAVLEGKIS-GKPKPSVKWYKNGEELKPSDRV--KIEN---- 3980

Qy        197 VNSETGTLVFNAVHKDDSGQYYCIASNDAG 226
Db       3981 LDDGTQRLTVTNAKLDDMDEYRCEASNEFG 4010


RESULT 13
T17346
hypothetical protein DKFZp586O1624.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17346
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Accession: T17346
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-483 <DUE>
A;Cross-references: EMBL:AL117666
A;Experimental source: adult uterus; clone DKFZp586O1624
C;Genetics:
A;Note: DKFZp586O1624.1

  Query Match             10.2%;  Score 166;  DB 2;  Length 483;
  Best Local Similarity   22.8%;  Pred. No. 8.1e-06;
  Matches   66;  Conservative   44;  Mismatches  101;  Indels   78;  Gaps   16;

Qy         51 LSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGR---------TDVFGKTSLR 101
Db          8 LECAATGH--PNPQIAWQK--DGGTDPP----------AARERRMHVMPDDDVFFITDVK 53

Qy        102 IWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP---AAVPVGKTATL 158
Db         54 I-----DDAGVYSC--TAQNSAGSISANATLTVLE----TPSLVVPLEDRVVSVGETVAL 102

Qy        159 QCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYY 218
Db        103 QC-KATGNPPPRITWFKGDRPLSLTER---------HHLTPDNQLLVVQNVVAEDAGRYT 152

Qy        219 CIASNDAGAARCEGQDMEVYDLNIAGIIG--------GVLVVLIVLAVI---TMGICCAY 267
Db        153 CEMSNTLGTERAHSQ------LSVLPAAGCRKDGTTVGIFTIAVVSSIVLTSLVWVCIIY 206

Qy        268 RRGCFISSKQDGESYKSPGKHDGV------NYIRTSEEGDFRHKSSFVI 310
Db        207 Q------TRKKSEEYSVTNTDETVVPPDVPSYL--SSQGTLSDRQETVV 247


RESULT 14
T33433
hypothetical protein T17A3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33433
R;Clarke, K.; Rohlfing, T.; Morris, M.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid T17A3.
A;Reference number: Z21343
A;Accession: T33433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-352 <CLA>
A;Cross-references: EMBL:AF078787; PIDN:AAC26956.1; GSPDB:GN00021; CESP:T17A3.10
A;Experimental source: strain Bristol N2; clone T17A3
C;Genetics:
A;Gene: CESP:T17A3.10
A;Map position: 3
A;Introns: 21/3; 112/3; 195/2; 341/2

  Query Match             10.1%;  Score 164.5;  DB 2;  Length 352;
  Best Local Similarity   22.8%;  Pred. No. 7.4e-06;
  Matches   61;  Conservative   57;  Mismatches   65;  Indels   85;  Gaps   17;

Qy         43 VHEFESVELSCIITHSQTSDPRIEWK---KIQDGQTTYVYFDNKIQGDLAGRTDVPGKTS 99
Db        143 VYEQDTVNLPCAIPHS-----AINWKVSWRLENSNST---------SDLSVTTLIDGNSK 188

Qy        100 LRIW---NVTRSDSAIYRCEVVA--LNDRKEVDEITIELIVQVKPVT----PVCRIPAAV 150
Db        189 YHVTTVKNITK--SGVYTCVIEADKFKERRQL----LETVIKVKPASTRPEPIKSSKMAI 242

Qy        151 PVGKTA---TLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
Db        243 PNCKSSIEIEIQCNIT-GHPLPEYSWVTDE-------------------SSGSTLTIS 280

Qy        208 AVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAG----IIGGVLVVLIVLAVITMGI 263
```

```
Db        281 ----EDSGVFQCIDSKN-----------RYVEVNVTGSHRKALGFYIIVALLMSV-TVGV 324

Qy        264 CCAYRRGCFISSKQ--DGESYKSPGKHD 289
              |       |: |::  :|   | | :::
Db        325 C------VFLISERVANGTEKKRPVQYN 346


RESULT 15
IJBONC
neural cell adhesion molecule short domain form precursor - bovine
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A;Reference number: A32976; MUID:89378239; PMID:2776887
A;Accession: A32976
A;Molecule type: mRNA
A;Residues: 1-853 <LIP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
A;Molecule type: protein
A;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A;Note: the authors identified this protein as calmodulin-independent adenylate cyclase
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: B44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Note: 23-Glu was also found
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F;20-719/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-288/Domain: immunoglobulin homology <IMM3>
F;261-270/Region: NCAM binding #status predicted
F;321-396/Domain: immunoglobulin homology <IMM4>
F;428-490/Domain: immunoglobulin homology <IMM5>
F;527-604/Domain: fibronectin type III repeat homology <FN3A>
F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transmembrane #status predicted <TMM>
F;738-853/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           10.1%;  Score 164.5;  DB 1;  Length 853;
  Best Local Similarity  25.5%;  Pred. No. 2.1e-05;
  Matches   59;  Conservative   42;  Mismatches   85;  Indels   45;  Gaps   12;

Qy         27 CMIEA---------VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :       |   ||   | : |:     :|  | | ||
Db         96 CVVTAEDGTESEATVNVKIFQKLMFKNAPTPQEFREGEDAVIVCDVVSSLPPTIIWK--H 153

Qy         72 DGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEI 129
               |:      |  :: |:  |  |      |:|  : ::|   ||||  ::|   | |::
Db        154 KGR------DVILKKDV--RPIVLTNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFK 202

Qy        130 TIELIVQVKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRAN 187
               |::|| | |     :  : |   :|:: || |  :||:| |  || ::   :  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-NAEGFPEPTVSWTKDGEQIENE---- 257

Qy        188 PRPQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                  ::  :  : ::  |    | |:|  :| ||| | ||      || ::
Db        258 ---EDEKYLPSDDSSELTIRKVDKNDEAEYVCIAENKAGE-----QDASIH 300


Search completed: June 15, 2004, 11:05:46
Job time : 16 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:51:49 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	505	30.9	298	1	JAM2_HUMAN	P57087 homo sapien
2	449.5	27.5	300	1	JAM1_MOUSE	O88792 mus musculu
3	415	25.4	299	1	JAM1_HUMAN	Q9y624 homo sapien
4	409.5	25.1	298	1	JAM1_BOVIN	Q9xt56 bos taurus
5	242.5	14.8	319	1	A33_HUMAN	Q99795 homo sapien
6	180	11.0	1088	1	NCA1_XENLA	P16170 xenopus lae
7	178	10.9	1051	1	PTK7_CHICK	Q91048 gallus gall
8	177	10.8	333	1	AMAL_DROME	P15364 drosophila
9	172.5	10.6	365	1	CXAR_HUMAN	P78310 homo sapien
10	172.5	10.6	837	1	NCM2_MOUSE	O35136 mus musculu
11	172.5	10.6	858	1	NCA1_RAT	P13596 rattus norv
12	170	10.4	349	1	LACH_SCHAM	Q26474 schistocerc
13	169.5	10.4	725	1	NCA2_MOUSE	P13594 mus musculu
14	169.5	10.4	1115	1	NCA1_MOUSE	P13595 mus musculu
15	169	10.3	1092	1	NCA2_XENLA	P36335 xenopus lae
16	167.5	10.3	837	1	NCM2_HUMAN	O15394 homo sapien
17	167.5	10.3	3707	1	PGBM_MOUSE	Q05793 mus musculu
18	167.5	10.3	6632	1	UN89_CAEEL	O01761 caenorhabdi
19	164.5	10.1	853	1	NCA1_BOVIN	P31836 bos taurus
20	163	10.0	344	1	NTRI_HUMAN	Q9p121 homo sapien
21	163	10.0	761	1	NCA2_HUMAN	P13592 homo sapien
22	163	10.0	848	1	NCA1_HUMAN	P13591 homo sapien
23	161	9.9	1377	1	NEO1_RAT	P97603 rattus norv
24	159.5	9.8	1277	1	CAML_FUGRU	Q98902 fugu rubrip
25	159	9.7	1091	1	NCA1_CHICK	P13590 gallus gall
26	157	9.6	344	1	NTRI_MOUSE	Q99pj0 mus musculu
27	156	9.6	344	1	NTRI_RAT	Q62718 rattus norv
28	156	9.6	1493	1	NEO1_MOUSE	P97798 mus musculu
29	155	9.5	353	1	CEPU_CHICK	Q90773 gallus gall
30	151.5	9.3	365	1	CXAR_MOUSE	P97792 mus musculu
31	151.5	9.3	873	1	FAS2_DROME	P34082 drosophila
32	151	9.2	1912	1	PTPD_HUMAN	P23468 homo sapien
33	150	9.2	1694	1	SN_MOUSE	Q62230 mus musculu
34	149.5	9.2	4391	1	PGBM_HUMAN	P98160 homo sapien
35	148.5	9.1	1070	1	PTK7_HUMAN	Q13308 homo sapien
36	148.5	9.1	1461	1	NEO1_HUMAN	Q92859 homo sapien
37	148	9.1	1040	1	AXO1_HUMAN	Q02246 homo sapien
38	148	9.1	1040	1	AXO1_RAT	P22063 rattus norv
39	147.5	9.0	847	1	CD22_HUMAN	P20273 homo sapien
40	145	8.9	359	1	LACH_DROME	Q24372 drosophila
41	144.5	8.8	702	1	CEA5_HUMAN	P06731 homo sapien
42	144	8.8	521	1	CEA1_MOUSE	P31809 mus musculu
43	143.5	8.8	1443	1	NEO1_CHICK	Q90610 gallus gall
44	143	8.8	345	1	OPCM_BOVIN	P11834 bos taurus
45	143	8.8	345	1	OPCM_RAT	P32736 rattus norv

ALIGNMENTS

RESULT 1
JAM2_HUMAN
ID JAM2_HUMAN STANDARD; PRT; 298 AA.
AC P57087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 2 precursor (Vascular endothelial
DE junction-associated molecule) (VE-JAM).
GN JAM2 OR VEJAM OR C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20507930; PubMed=10945976;
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J.,
RA Vanderslice P., Morris A.P., Brock T.A.;
RT "A novel protein with homology to the junctional adhesion molecule:
RT Characterization of leukocyte interactions.";
RL J. Biol. Chem. 275:34750-34756(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC       SECONDARY LYMPHOID ORGANS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC       VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC       LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC       CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3(2001);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF255910; AAF81223.1; -.
DR   EMBL; AY016009; AAG49022.1; -.
DR   EMBL; BC017779; AAH17779.1; -.
DR   Genew; HGNC:14686; JAM2.
DR   MIM; 606870; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1    20       POTENTIAL.
FT   CHAIN        21   298       JUNCTIONAL ADHESION MOLECULE 2.
FT   DOMAIN       21   238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239   259       POTENTIAL.
FT   DOMAIN      260   298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32   127       IG-LIKE V-TYPE.
FT   DOMAIN      134   238       IG-LIKE C2-TYPE.
FT   DISULFID     50   109       POTENTIAL.
FT   DISULFID    155   214       POTENTIAL.
FT   CARBOHYD     98    98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187   187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    236   236       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  33207 MW;  CA78E518E22DCAEE CRC64;

  Query Match             30.9%;  Score 505;  DB 1;  Length 298;
  Best Local Similarity   37.3%;  Pred. No. 9.7e-36;
  Matches  118;  Conservative   61;  Mismatches  111;  Indels   26;  Gaps    9;

Qy          3 LSRRLRLRLYARLPHFFLLLLFRGCMI-----EAVNLKSSNRNPVVH--EFESVELSCII 55
              ::|| | ||         |||| |  ::     :|    :      ||   |::   |:|
Db          1 MARRSRHRL--------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51

Qy         56 THSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRC 115
                |  :|   |:||||:     ::||:   :|||    | ::    ::|| ||||||:  |||
Db         52 TPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC 109

Qy        116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
              || | ::: : ::| |: | | | |  | | :|::   |    |:||: || | | |:|:
Db        110 EVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF 169

Qy        175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
              :: : |  : |   :  |||: :|::|||| || | | |:|:| | | |  | || |:
Db        170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR 229

Qy        235 MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYI 294
              |:| ||||:|||  |:|| :|::|  :|:| | |:| |  ||:       |  | :  :
Db        230 MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE-----TSFQKSNSSSKA 282

Qy        295 RTSEEGDFRHKSSFVI 310

                |  | ||:|  ||:|
Db        283 TTMSENDFKHTKSPII 298


RESULT 2
JAM1_MOUSE
ID   JAM1_MOUSE     STANDARD;      PRT;   300 AA.
AC   O88792;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1 OR JCAM1 OR JCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98327120; PubMed=9660867;
RA   Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA   Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA   Simmons D., Dejana E.;
RT   "Junctional adhesion molecule, a novel member of the immunoglobulin
RT   superfamily that distributes at intercellular junctions and modulates
RT   monocyte transmigration.";
RL   J. Cell Biol. 142:117-127(1998).
RN   [2]
RP   INTERACTION WITH PARD3.
RX   MEDLINE=21340266; PubMed=11447115;
RA   Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA   Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
RT   "The cell polarity protein ASIP/PAR-3 directly associates with
RT   junctional adhesion molecule (JAM).";
RL   EMBO J. 20:3738-3748(2001).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX   MEDLINE=21391702; PubMed=11500366;
RA   Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA   Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA   Winkler F.K., Hennig M.;
RT   "X-ray structure of junctional adhesion molecule: structural basis for
RT   homophilic adhesion via a novel dimerization motif.";
RL   EMBO J. 20:4391-4398(2001).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly. Plays a role in regulating monocyte
CC       transmigration involved in integrity of epithelial barrier.
CC       Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC       Localized at tight junctions of both epithelial and endothelial
CC       cells.
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U89915; AAC32982.1; -.
DR   PDB; 1F97; 22-AUG-01.
DR   MGD; MGI:1321398; F11r.
```

```
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal; 3D-structure.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    300       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       27    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    122       IG-LIKE V-TYPE 1.
FT   DOMAIN      134    230       IG-LIKE V-TYPE 2.
FT   DISULFID     49    108       POTENTIAL.
FT   DISULFID    152    212       POTENTIAL.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32368 MW;  391F3E48FF3B97EC CRC64;

  Query Match             27.5%;  Score 449.5;  DB 1;  Length 300;
  Best Local Similarity   34.2%;  Pred. No. 5.2e-31;
  Matches  102;  Conservative   64;  Mismatches  117;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCMIEAV-----NLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQ 74
Db         11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELI 134
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT-DSRANPRFQNS 193
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
Db        247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 3
JAM1_HUMAN
ID   JAM1_HUMAN     STANDARD;      PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
DE   molecule 1) (PAM-1) (Platelet F11 receptor) (UNQ264/PRO301).
GN   F11R OR JAM1 OR JCAM.
OS   Homo sapiens (Human).
OC   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA   Kornecki E.;
RT   "Molecular cloning and sequencing of the cDNA of F11 receptor, a
RT   novel Ig superfamily member from human platelets.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Naik U.P., Naik M.U., DeLeon P., Spychala J.;
RT   "Cloning and characterization of PAM-1, a novel platelet adhesion
RT   molecule involved in platelet activation.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
```

```
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111713; AAD42050.1; -.
DR   EMBL; AF207907; AAF22829.1; -.
DR   EMBL; AF172398; AAD48877.1; -.
DR   EMBL; AL136649; CAB66584.1; -.
DR   EMBL; AY358896; AAQ89255.1; -.
DR   EMBL; BC001533; AAH01533.1; -.
DR   PIR; A59406; S56749.
DR   Genew; HGNC:14685; F11R.
DR   MIM; 605721; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    299       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       26    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       27    125       IG-LIKE V-TYPE 1.
FT   DOMAIN      135    228       IG-LIKE V-TYPE 2.
FT   DISULFID     50    109       POTENTIAL.
FT   DISULFID    153    212       POTENTIAL.
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   299 AA;  32583 MW;  D95DE2FEA23D2851 CRC64;

  Query Match             25.4%;  Score 415;  DB 1;  Length 299;
  Best Local Similarity   33.8%;  Pred. No. 4.4e-28;
  Matches  100;  Conservative   50;  Mismatches  132;  Indels   14;  Gaps    6;

Qy         18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
              | | :|     : :| : ||      : |   |:|||   :|  | ||:|||  |   |
Db         15 PILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy         78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
              | ::|||      |   |  | :   :||| |:  | | :|:        |: ::||| |
Db         73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy        138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
              |  |    ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db        131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy        198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
              |  || |||: :   |:|:| | | |  |         ||  : |:  |:  ||| ||:|
Db        191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy        257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
               ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db        251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299


RESULT 4
JAM1_BOVIN
ID   JAM1_BOVIN     STANDARD;      PRT;   298 AA.
AC   Q9XT56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111714; AAD42051.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    298       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       25    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    124       IG-LIKE V-TYPE 1.
FT   DOMAIN      134    227       IG-LIKE V-TYPE 2.
FT   DISULFID     49    108       POTENTIAL.
FT   DISULFID    152    211       POTENTIAL.
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  32456 MW;  714FE1C1714769A2 CRC64;

  Query Match             25.1%;  Score 409.5;  DB 1;  Length 298;
  Best Local Similarity   32.3%;  Pred. No. 1.3e-27;
  Matches   97;  Conservative   53;  Mismatches  127;  Indels   23;  Gaps    8;

Qy         21 LLLFRGCMIEAVNL---KSSNRNPVVH--EFESVELSCIITHSQTSDPRIEWKKIQDGQT 75
              ||||   :: :: |         |||    |    :|||  ::|  | ||:|||
Db         12 LLLFTSMILCSLALGRGAVQTYEPVVRVPENNPAKLSC--SYSGFSSPRVEWKFTHGDIR 69

Qy         76 TYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIV 135
              | ::|||      |   |  | :   :||| |: :| | :|:        |:|::|||
Db         70 GLVCYNNKITASYENRV-TFSDTGITFHSVTRKDTGMYTC-MVSDEGGNTYGEVTVQLIV 127

Qy        136 QVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSF 195
              | |  |   :|::| :|  | | | | :| |    | |::: | :| : ::|  | |||:
```

```
Db        128 LVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEPKSNRAPSNSSY 187

Qy        196 HVNSETGTLVFNAVHKDDSGQYYCIASND-AGAARCEGQDMEVYDLNIAGIIGGVLVVLI 254

Db        188 TLNQKTGELIFDPVSASDTGDFTCQAQNGYASPVKSDTVHMDAVELNVGGIVAAVFVTLI 247

Qy        255 VLAVITMGICCAYRRGCFISSKQDGES----YKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310

Db        248 LLGALIFGIWFAYSRGYFDRAKKGTSNKKVIYSQP---------NARSDGEFRQTSSFLV 298


RESULT 5
A33_HUMAN
ID   A33_HUMAN      STANDARD;      PRT;   319 AA.
AC   Q99795;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cell surface A33 antigen precursor (Glycoprotein A33).
GN   GPA33.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=97165045; PubMed=9012807;
RA   Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA   Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA   Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA   Burgess A.W.;
RT   "The human A33 antigen is a transmembrane glycoprotein and a novel
RT   member of the immunoglobulin superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN   [2]
RP   POST-TRANSLATIONAL MODIFICATIONS.
RX   MEDLINE=97396159; PubMed=9245713;
RA   Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA   Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA   Simpson R.J.;
RT   "Characterization of posttranslational modifications of human A33
RT   antigen, a novel palmitoylated surface glycoprotein of human
RT   gastrointestinal epithelium.";
RL   Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC   -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC       epithelium and in 95% of colon cancers.
CC   -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC       CARBOHYDRATE.
CC   -!- PTM: Palmitoylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U79725; AAC50957.1; -.
DR   Genew; HGNC:4445; GPA33.
DR   MIM; 602171; -.
DR   GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW   Transmembrane; Signal; Antigen.
FT   SIGNAL        1     21
FT   CHAIN        22    319       CELL SURFACE A33 ANTIGEN.
FT   DOMAIN       22    235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    236    256       POTENTIAL.
FT   DOMAIN      257    319       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       22    134       IG-LIKE V-TYPE.
FT   DOMAIN      140    227       IG-LIKE C2-TYPE.
FT   DOMAIN      258    261       POLY-CYS.
FT   DISULFID     43    117       POTENTIAL.
FT   DISULFID    146    222       POTENTIAL.
FT   DISULFID    162    211       POTENTIAL.
FT   CARBOHYD    112    112       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   319 AA;  35632 MW;  9BFC7AAF45C2408E CRC64;

  Query Match          14.8%;  Score 242.5;  DB 1;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 2.3e-13;
  Matches   80;  Conservative   49;  Mismatches  123;  Indels   59;  Gaps   12;

Qy         29 IEAVNLKSSNRNPVVHEPESVELSCIITHSQTS--DPRIEWKKIQDGQTTYVY---PDNK 83

Db         19 VDAISVETPQDVLRASQGKSVTLPCTY-HTSTSSREGLIQWDKLLLTHTERVVIWPFSNK 77

Qy         84 --IQGDL----------AGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITI 131

Db         78 NYIHGELYKNRVSISNNAEQSD----ASITIDQLTMADNGTYECSVSLMSDLEGNTKSRV 133

Qy        132 ELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDV-----PLPTDSRA 186

Db        134 RLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASG 193

Qy        187 NPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAG--------AARCEGQDMEVY 238

Db        194 QP--------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALY 238

Qy        239 DLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDG----ESYKSPGKHDGVNYI 294

Db        239 ----VGIAVGVVAALIIIGII-IYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR 293

Qy        295 RTSEEGDFRHK 305

Db        294 ERKEEDDYRQE 304


RESULT 6
NCA1_XENLA
ID   NCA1_XENLA     STANDARD;      PRT;  1088 AA.
AC   P16170;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).
RX   MEDLINE=90098871; PubMed=2481269;
RA   Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT   "Primary structure and developmental expression of a large
RT   cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT   molecule (NCAM).";
RL   Nucleic Acids Res. 17:10321-10335(1989).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
```

```
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=N-CAM 180;
CC         IsoId=P16170-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P16170-2; Sequence=VSP_002589;
CC   -!- TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
CC       tissue.
CC   -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC       TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC       EARLY NEURAL DEVELOPMENT.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M25696; AAA49909.1; -.
DR   PIR; S09600; IJXLNL.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20   1088       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1088       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      209    294       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    484       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    804   1049       Missing (in isoform N-CAM 140).
FT                                /FTId=VSP_002589.
SQ   SEQUENCE   1088 AA;  117778 MW;  62738B55B03F3E83 CRC64;

  Query Match             11.0%;  Score 180;  DB 1;  Length 1088;
  Best Local Similarity   28.8%;  Pred. No. 2.2e-07;
  Matches   60;  Conservative   33;  Mismatches   81;  Indels   34;  Gaps   11;

Qy         32 VNLK-----SSNRNPVVHEPESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
               ||||     :    |  ||:  | : ||    :| |  | |: | :|     | |   :
Db        107 VNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                  | |     |:|  : ::|   ||||  ::|   | |::   |::|| | |
Db        162 ------RFVVLANNYLQIRGIKKTDEGTYRCEGRILA---RGEINYKDIQVIVNVPPTIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
               |: |   : ::  | | :::|:| |  || :  |:          :  ||  | :
Db        213 ARQLRVNATANMAESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :  : | |||  :| |||:| || |
Db        264 QSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 7
PTK7_CHICK
ID   PTK7_CHICK     STANDARD;      PRT;  1051 AA.
AC   Q91048;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tyrosine-protein kinase-like 7 precursor (Kinase like protein).
GN   PTK7 OR KLG.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic brain;
RX   MEDLINE=91271300; PubMed=1711213;
RA   Chou Y.-H., Hayman M.J.;
RT   "Characterization of a member of the immunoglobulin gene superfamily
RT   that possibly represents an additional class of growth factor
RT   receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).
CC   -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
CC       THE CATALYTIC ACTIVITY OF TYROSINE KINASE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA,
CC       THYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLASTS. ALSO EXPRESSED
CC       IN EMBRYONIC LIVER.
CC   -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63437; AAA48933.1; -.
DR   PIR; A39712; A39712.
DR   HSSP; P12931; 1FMK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 7.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 4.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 7.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
```

```
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23   1051       TYROSINE-PROTEIN KINASE-LIKE 7.
FT   DOMAIN       23    685       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    686    706       POTENTIAL.
FT   DOMAIN      707   1051       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    105       IG-LIKE C2-TYPE 1.
FT   DOMAIN      115    204       IG-LIKE C2-TYPE 2.
FT   DOMAIN      213    298       IG-LIKE C2-TYPE 3.
FT   DOMAIN      308    388       IG-LIKE C2-TYPE 4.
FT   DOMAIN      393    472       IG-LIKE C2-TYPE 5.
FT   DOMAIN      487    566       IG-LIKE C2-TYPE 6.
FT   DOMAIN      573    661       IG-LIKE C2-TYPE 7.
FT   DOMAIN      777   1048       PROTEIN KINASE; INACTIVE.
FT   DISULFID     40     88       BY SIMILARITY.
FT   DISULFID    137    187       BY SIMILARITY.
FT   DISULFID    234    282       BY SIMILARITY.
FT   DISULFID    326    372       BY SIMILARITY.
FT   DISULFID    414    462       BY SIMILARITY.
FT   DISULFID    505    551       BY SIMILARITY.
FT   DISULFID    594    645       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    264    264       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    444    444       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    548    548       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1051 AA;  116366 MW;  1752442AEA4CB702 CRC64;

  Query Match             10.9%;  Score 178;  DB 1;  Length 1051;
  Best Local Similarity   28.3%;  Pred. No. 3.2e-07;
  Matches   72;  Conservative   29;  Mismatches  109;  Indels   44;  Gaps   12;

Qy         45 EP-ESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIW 103
              || : | :||  |  :   | |:| |  ||       : :   :: |  :     |
Db        496 EFNKEVTVSCSATGRE--KPTIQWTK-TDG--------SSLPSHVSHRAGI-----LSFH 539

Qy        104 NVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQES 163
               |:||||  | |  :| |  :     |::|:| |     :   |  |  | ||  ||| :
Db        540 KVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVYVTFKLEPEPTTVYQGHTAMFQCQ-A 596

Qy        164 EGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASN 223
              || | ||  |   | |  |:  || |          |:||   |  :|||:| ||| |
Db        597 EGDPVPHIQWKGKDKIL-DPSKLLPRIQ------IMPNGSLVIYDVTTEDSGKYTCIAGN 649

Qy        224 DA--------------GAARCEGQDMEV-YD-LNIAGIIGGVLVVLIVLAVITMGICCA 266
                           |  ||      |  :  |:  |  |  |:: :  |  |
Db        650 SCNIKHREAFLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIIIVLGLMFYCKK 709

Qy        267 YRRGCFISSKQDGE 280
               |:   :    :||
Db        710 RRKAKRLKKHPEGE 723


RESULT 8
AMAL_DROME
ID   AMAL_DROME     STANDARD;      PRT;   333 AA.
AC   P15364; Q9V3A5;
DT   01-APR-1990 (Rel. 14, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amalgam protein precursor.
GN   AMA OR BG:DS00276.6 OR CG2198.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=89028670; PubMed=3141062;
RA   Seeger M.A., Haffley L., Kaufman T.C.;
RT   "Characterization of amalgam: a member of the immunoglobulin
RT   superfamily from Drosophila.";
RL   Cell 55:589-600(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA   Palazzolo M.J.;
RT   "Complete sequence of the Antennapedia complex of Drosophila.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
```

```
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; M23561; AAA28367.1; -.
DR   EMBL; AE001572; AAD19797.1; -.
DR   EMBL; AE003674; AAF54084.1; -.
DR   EMBL; AY051911; AAK93335.1; -.
DR   PIR; A31923; A31923.
DR   FlyBase; FBgn0000071; Ama.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
KW   Repeat.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24      ?       AMALGAM PROTEIN.
FT   PROPEP        ?    333       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       25    128       IG-LIKE V-TYPE.
FT   DOMAIN      139    223       IG-LIKE C2-TYPE 1.
FT   DOMAIN      230    323       IG-LIKE C2-TYPE 2.
FT   DISULFID     46    117       PROBABLE.
FT   DISULFID    161    208       PROBABLE.
FT   DISULFID    251    307       PROBABLE.
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     83     83       Q -> K (IN REF. 1).
SQ   SEQUENCE   333 AA;  36387 MW;  F644753DE3DB25F1 CRC64;

  Query Match             10.8%;  Score 177;  DB 1;  Length 333;
  Best Local Similarity   27.2%;  Pred. No. 9.2e-08;
  Matches   53;  Conservative   38;  Mismatches   82;  Indels   22;  Gaps    6;

Qy         35 KSSNRNPVVHEFESVELSCIITHSQ-TSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTD 93
              ::: :: :| | :::||:|   |:     | | | :  :               :
Db        143 ENTPKSTLVTEGQNLELTC---HANGFPKPTISWAREHNAV------------MPAGGH 186

Qy         94 VFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVG 153
              :  : :||| :| | |   | | :| |  : |:  | : |: :|   | |   | |
Db        187 LLAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVS 244

Qy        154 KTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDD 213
              :| |:|   :||| |   |::| |||   |  :    |::   : |  |  ::| ::|
Db        245 HSAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEED 301

Qy        214 SGQYYCIASNDAGAA 228
              | ||| |:|  | |
Db        302 FGDYYCNATNKLGHA 316


RESULT 9
CXAR_HUMAN
ID   CXAR_HUMAN     STANDARD;      PRT;   365 AA.
AC   P78310; O00694;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE   adenovirus receptor) (hCAR) (CVB3 binding protein).
GN   CXADR OR CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97190109; PubMed=9036860;
RA   Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA   Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT   "Isolation of a common receptor for Coxsackie B viruses and
RT   adenoviruses 2 and 5.";
RL   Science 275:1320-1323(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97250541; PubMed=9096397;
RA   Tomko R.P., Xu R., Philipson L.;
RT   "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT   adenoviruses and group B coxsackieviruses.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20008750; PubMed=10543405;
RA   Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA   Bowles N.E.;
RT   "Genomic organization and chromosomal localization of the human
RT   Coxsackievirus B-adenovirus receptor gene.";
RL   Hum. Genet. 105:354-359(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
RT   "Sequence and expression of CXADR, the human gene for the
RT   coxsackievirus and adenovirus receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
RA   Sollerbrant K., Sonnhammer E., Philipson L.;
RT   "Putative regulatory domains in the human and mouse CAR genes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervix;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC       SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; Y07593; CAA68868.1; -.
DR   EMBL; U90716; AAC51234.1; -.
DR   EMBL; AF169366; AAF05908.1; -.
DR   EMBL; AF169360; AAF05908.1; JOINED.
DR   EMBL; AF169361; AAF05908.1; JOINED.
DR   EMBL; AF169362; AAF05908.1; JOINED.
```

```
DR   EMBL; AF169363; AAF05908.1; JOINED.
DR   EMBL; AF169364; AAF05908.1; JOINED.
DR   EMBL; AF169365; AAF05908.1; JOINED.
DR   EMBL; AF200465; AAF24344.1; -.
DR   EMBL; AF242865; AAG01088.1; -.
DR   EMBL; AF242862; AAG01088.1; JOINED.
DR   EMBL; AF242864; AAG01088.1; JOINED.
DR   EMBL; BC003684; AAH03684.1; -.
DR   EMBL; BC010536; AAH10536.1; -.
DR   PDB; 1EAJ; 13-JUL-01.
DR   PDB; 1F5W; 08-NOV-00.
DR   PDB; 1KAC; 24-NOV-99.
DR   Genew; HGNC:2559; CXADR.
DR   MIM; 602621; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Repeat; 3D-structure.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    365       COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT   DOMAIN       20    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    365       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    134       IG-LIKE C2-TYPE 1.
FT   DOMAIN      141    228       IG-LIKE C2-TYPE 2.
FT   DISULFID     41    120       BY SIMILARITY.
FT   DISULFID    162    212       BY SIMILARITY.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   365 AA;  40029 MW;  AB01C6346CB7FE64 CRC64;

  Query Match             10.6%;  Score 172.5;  DB 1;  Length 365;
  Best Local Similarity   25.9%;  Pred. No. 2.5e-07;
  Matches   68;  Conservative   38;  Mismatches  116;  Indels   41;  Gaps   11;

Qy         47 ESVELSCIITHS-QTSDP-RIEW-------KKIQDGQTTYVYFDNKIQG----DLAGRTD 93
              |:  | |  | | :   |  |||        :|:   |   :|  :||       || ||
Db         35 ETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVD--QVIILYSGDKIYDDYYPDLKGRVH 92

Qy         94 V------FGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP 147
                    |  |: : |:  ||   |:|:|        |     | |:| |||    | :
Db         93 FTSNDLKSGDASINVTNLQLSDIGTYQCKV---KKAPGVANKKIHLVVLVKPSGARCYVD 149

Qy        148 AAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
               :  :|    ::|:  ||      | | :      :||:  |   :|:     :  :
Db        150 GSEEIGSDFKIKCEPKEGSLPLQYEWQK-----LSDSQKMP----TSWLAEMTSSVISVK 200

Qy        208 AVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLV-VLIVLAVITMGICCA 266
                : || | |   |  |: :|  :   |   | ||:| | ::  |: ||:| : | |
Db        201 NASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCC 260

Qy        267 YRRGCFISSKQDGESYKSPGKHD 289
               :       |:  | |:    ||
Db        261 RK-------KRREEKYEKEVHHD 276


RESULT 10
NCM2_MOUSE
ID   NCM2_MOUSE     STANDARD;      PRT;   837 AA.
AC   O35136; O35962;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE   adhesion molecule) (R4B12).
GN   NCAM2 OR OCAM OR RNCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC   STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX   MEDLINE=97368238; PubMed=9221781;
RA   Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA   Kagamiyama H., Mori K.;
RT   "OCAM: A new member of the neural cell adhesion molecule family
RT   related to zone-to-zone projection of olfactory and vomeronasal
RT   axons.";
RL   J. Neurosci. 17:5830-5842(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX   MEDLINE=97476194; PubMed=9334170;
RA   Alenius M., Bohm S.;
RT   "Identification of a novel neural cell adhesion molecule-related gene
RT   with a potential role in selective axonal projection.";
RL   J. Biol. Chem. 272:26083-26086(1997).
CC   -!- FUNCTION: May play important roles in selective fasciculation and
CC       zone-to-zone projection of the primary olfactory axons.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC       attached to the membrane by a GPI-anchor (short isoform).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=O35136-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=O35136-2; Sequence=VSP_002590;
CC   -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC       vomeronasal neurons in a zone-specific manner.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF001287; AAB69125.1; -.
DR   EMBL; AF001286; AAB69124.1; -.
DR   EMBL; AF016619; AAC53375.1; -.
DR   MGD; MGI:97282; Ncam2.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW   Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    837       NEURAL CELL ADHESION MOLECULE 2.
FT   DOMAIN       20    697       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    698    718       POTENTIAL.
FT   DOMAIN      719    837       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    297       IG-LIKE C2-TYPE 3.
FT   DOMAIN      302    396       IG-LIKE C2-TYPE 4.
FT   DOMAIN      401    491       IG-LIKE C2-TYPE 5.
FT   DOMAIN      482    581       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      594    678       FIBRONECTIN TYPE-III 2.
FT   DISULFID     42     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    281       PROBABLE.
```

```
FT   DISULFID    322    380       PROBABLE.
FT   DISULFID    422    475       PROBABLE.
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    309    309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    419    419       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    445    445       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    474    474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    562    562       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    694    837       TLFNGLGLGAIIGLGVAALLLILVVTDVSCFFIRQCGLLMC
FT                                ITRRMCGKKSGSSGKSKELEEGKAAYLKDGSKEPIVEMRTE
FT                                DERITNHEDGSPVNEPNETTPLTEPEKLPLKEENGKEVLNA
FT                                ETIEIKVSNDIIQSKEDDIKA -> NCCEANKGENGGQSWH
FT                                LNAVGFTFVITMSLSCLF (in isoform Short).
FT                                /FTId=VSP_002590.
SQ   SEQUENCE   837 AA;  93203 MW;  70473B053A2D65A5 CRC64;

  Query Match             10.6%;  Score 172.5;  DB 1;  Length 837;
  Best Local Similarity   30.1%;  Pred. No. 7e-07;
  Matches   55;  Conservative   26;  Mismatches   75;  Indels   27;  Gaps    8;

Qy         47 ESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVT 106
              |  |: | :: |    | : |          :| : ::       |  |    :|:| |:
Db        130 EDAEVVCRVSSSPA--PAVSW----------LYHNEEVTTIPDNRFAVLANNNLQILNIN 177

Qy        107 RSDSAIYRCEVVALNDRKEVDEITIELIVQVKP--VTPVCRIPAAVPVGKTATLQCQESE 164
              :||  |||||   :  | |:|   | :|| | |  : |      |    |:  || |: |
Db        178 KSDEGIYRCE-GRVEARGEIDFRDIIIVIVNVPPAIMMPQKSFNATAERGEEMTLTCKAS- 235

Qy        165 GYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV-NSETGTLVFNAVHKDDSGQYYCIASN 223
              | | |  ||:||   :          :|  : :  | |   | | ::| | | | | |:|
Db        236 GSPDPTISWFRNGKLIB---------ENEKYILKGSNTELTVRNIINK-DGGSYVCKATN 285

Qy        224 DAG 226
               ||
Db        286 KAG 288


RESULT 11
NCA1_RAT
ID   NCA1_RAT       STANDARD;      PRT;   858 AA.
AC   P13596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE   (NCAM-140).
GN   NCAM1 OR NCAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88059265; PubMed=3680385;
RA   Small S.J., Shull G.E., Santoni M.-J., Akeson R.;
RT   "Identification of a cDNA clone that contains the complete coding
RT   sequence for a 140-kD rat NCAM polypeptide.";
RL   J. Cell Biol. 105:2335-2345(1987).
RN   [2]
RP   SEQUENCE OF 355-364 FROM N.A.
RX   MEDLINE=90166485; PubMed=2483093;
RA   Small S.J., Haines S.L., Akeson R.A.;
RT   "Polypeptide variation in an N-CAM extracellular immunoglobulin-like
RT   fold is developmentally regulated through alternative splicing.";
RL   Neuron 1:1007-1017(1988).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC           IsoId=P13596-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X06564; CAA29809.1; -.
DR   EMBL; M32611; AAA41679.1; -.
DR   PIR; S00846; IJRTNC.
DR   PDB; 1EPF; 27-OCT-00.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
KW   3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    858       NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT                                 ISOFORM.
FT   DOMAIN       20    721       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    722    739       POTENTIAL.
FT   DOMAIN      740    858       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    414       IG-LIKE C2-TYPE 4.
FT   DOMAIN      417    502       IG-LIKE C2-TYPE 5.
FT   DOMAIN      514    615       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      616    712       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       BY SIMILARITY.
FT   DISULFID    139    189       BY SIMILARITY.
FT   DISULFID    235    288       BY SIMILARITY.
FT   DISULFID    330    396       BY SIMILARITY.
FT   DISULFID    437    490       BY SIMILARITY.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    460    460       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   858 AA;  94658 MW;  EA1A06A4EA0550F6 CRC64;

  Query Match             10.6%;  Score 172.5;  DB 1;  Length 858;
  Best Local Similarity   27.1%;  Pred. No. 7.2e-07;
  Matches   61;  Conservative   43;  Mismatches   84;  Indels   37;  Gaps   13;

Qy         26 GCMIEA-VNLKSSNR-----NPVVHEFESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
              |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db        103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy         79 YFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
              |  :: |:  | |      |:|  : ::|   ||||  ::|   | |::   |::||
Db        157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy        137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
              | |      :  : |   :|:: || | :::|:| |  || ::  |:  :       ::
```

```
Db        210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE------EDDE 262

Qy        195 FHV-NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
Db        263 KHIFSDDSSELTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302


RESULT 12
LACH_SCHAM
ID   LACH_SCHAM     STANDARD;      PRT;   349 AA.
AC   Q26474;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Lachesin precursor.
GN   LAC.
OS   Schistocerca americana (American grasshopper).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX   NCBI_TaxID=7009;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=94038693; PubMed=8223276;
RA   Karlstrom R.O., Wilder L.P., Bastiani M.J.;
RT   "Lachesin: an immunoglobulin superfamily protein whose expression
RT   correlates with neurogenesis in grasshopper embryos.";
RL   Development 118:509-522(1993).
CC   -!- FUNCTION: MAY PLAY A ROLE IN EARLY NEURONAL DIFFERENTIATION AND
CC       AXON OUTGROWTH.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: EXPRESSED BY ALL NEUROGENIC CELLS EARLY, BUT
CC       ONLY THOSE CELLS THAT BECOME NEUROBLASTS CONTINUE TO EXPRESS IT.
CC       EXPRESSED BY NEUROBLASTS, GANGLION MOTHER CELLS AND NEURONS EARLY
CC       IN THEIR LIVES, BUT EXPRESSION BECOMES RESTRICTED TO A SUBSET OF
CC       NEURONS AS DEVELOPMENT PROGRESSES. EXPRESSED BY SENSORY NEURONS AS
CC       THEY DELAMINATE FROM THE BODY WALL ECTODERM. IT IS ALSO PRESENT ON
CC       GROWING AXONS OF THE CNS AND PNS AND BECOMES RESTRICTED TO A
CC       SUBSET OF AXONS LATER IN DEVELOPMENT.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED ON DIFFERENTIATING NEURONAL CELLS
CC       FROM THE ONSET OF NEUROGENESIS IN BOTH THE CENTRAL AND PERIPHERAL
CC       NERVOUS SYSTEMS.
CC   -!- PTM: The N-terminus is blocked.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L13256; AAC37185.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal; Lipoprotein.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    332       LACHESIN.
FT   PROPEP      333    349       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       22    127       IG-LIKE V-TYPE.
FT   DOMAIN      132    218       IG-LIKE C2-TYPE 1.
FT   DOMAIN      222    315       IG-LIKE C2-TYPE 2.
FT   DISULFID     43    110       POTENTIAL.
FT   DISULFID    154    201       POTENTIAL.
FT   DISULFID    244    299       POTENTIAL.
FT   CARBOHYD    137    137       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       332    332       GPI-anchor amidated glycine (Potential).
SQ   SEQUENCE   349 AA;  38974 MW;  5F139A44BF849689 CRC64;

  Query Match             10.4%;  Score 170;  DB 1;  Length 349;
  Best Local Similarity   25.3%;  Pred. No. 3.8e-07;
  Matches   63;  Conservative   39;  Mismatches   73;  Indels   74;  Gaps   14;

Qy          9 LRLYARLPHFFLLLLPRGCMIEAVNLKSSNRNPVVHEFE---------SVELSCIITHSQ 59
Db          3 LRLYTIFVGPFSVVY------------AQRTPTISYISQEQIKDIGGTVELECSVQYAQ 49

Qy         60 TSDPRIEWKKIQDGQ----------TTYVYFDNKIQGDLAGRTDVFGKT-SLRIWNVTRS 108
Db         50 --DYPVLWMKVDRNRQVDPLPISTGSSLIIRDSR----FALRYDTASSTYTLQIKDIQET 103

Qy        109 DSAIYRCEV-VALNDRKEVDEITIELIVQVKPVTPVCRIPA---------AVPVGKTATL 158
Db        104 DAGFYQCQVIIGLNNK-----ITAEVDLQVR------RPPVISDNSTRSLVVSEGQAVRL 152

Qy        159 QCQESEGYPRPHYSWYR-NDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQY 217
Db        153 ECY-AGGYPAPRVSWRRENNAILPTG--------GSIYRGN----VLKISRIGKEDRGTY 199

Qy        218 YCIASNDAG 226
Db        200 YCVAENGVG 208


RESULT 13
NCA2_MOUSE
ID   NCA2_MOUSE     STANDARD;      PRT;   725 AA.
AC   P13594; Q61950;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE   (NCAM-120).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
RA   Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 20-700 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [3]
RP   SEQUENCE OF 642-725 FROM N.A.
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
```

```
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=Displayed;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=External;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00051; CAA68263.1; -.
DR   EMBL; X15049; CAA33148.1; ALT_SEQ.
DR   EMBL; X07195; CAA30173.1; -.
DR   PIR; A29673; IJMSNG.
DR   PDB; 2NCM; 12-MAR-97.
DR   PDB; 3NCM; 23-JUL-99.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
KW   Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
KW   3D-structure.
FT   SIGNAL       1     19
FT   CHAIN       20    725       NEURAL CELL ADHESION MOLECULE 1, 120 kDa
FT                               ISOFORM.
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
FT   DISULFID    139    189       PROBABLE.
FT   DISULFID    235    288       PROBABLE.
FT   DISULFID    330    386       PROBABLE.
FT   DISULFID    427    480       PROBABLE.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    261    268       ERSRSSVS -> DEKHIFSD (IN REF. 2).
FT   CONFLICT    273    273       V -> L (IN REF. 2).
FT   CONFLICT    354    355       QD -> KT (IN REF. 2).
FT   CONFLICT    549    549       T -> K (IN REF. 2).
FT   CONFLICT    572    572       T -> R (IN REF. 2).
FT   CONFLICT    575    575       D -> V (IN REF. 2).
FT   CONFLICT    589    594       MQPSES -> SAATEF (IN REF. 2).
FT   CONFLICT    600    602       PEL -> REP (IN REF. 2).
FT   CONFLICT    657    657       H -> D (IN REF. 2 AND 3).
SQ   SEQUENCE   725 AA;  80296 MW;  C2ABB8B4461C6B2F CRC64;

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 725;
  Best Local Similarity   27.7%;  Pred. No. 1e-06;
  Matches   62;  Conservative   43;  Mismatches   84;  Indels   35;  Gaps   13;

Qy         26 GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
              |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db        103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy         79 YFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
                 | :: |:  |  |      |:|  : ::|   ||||  ::|   | |::   |::||
Db        157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy        137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
              | |     :  : |   :|:: || | :::|:| |  || ::  |:  :   : | ::|
Db        210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE-DERSRSSV 267

Qy        195 FHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                |::  :    | |:|  :| ||| | ||      ||  ::
Db        268 ----SDSSEVTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302


RESULT 14
NCA1_MOUSE
ID   NCA1_MOUSE     STANDARD;      PRT;  1115 AA.
AC   P13595; Q61949;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
DE   (NCAM-180).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.;
RA   Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6;
RX   MEDLINE=88067687; PubMed=3684567;
RA   Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,
RA   Goridis C., Wille W.;
RT   "Analysis of cDNA clones that code for the transmembrane forms of the
RT   mouse neural cell adhesion molecule (NCAM) and are generated by
RT   alternative RNA splicing.";
RL   Nucleic Acids Res. 15:8621-8641(1987).
RN   [3]
RP   SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=88247737; PubMed=2454455;
RA   Barthels D., Vopper G., Wille W.;
RT   "NCAM-180, the large isoform of the neural cell adhesion molecule of
RT   the mouse, is encoded by an alternatively spliced transcript.";
RL   Nucleic Acids Res. 16:4217-4225(1988).
RN   [5]
```

```
RP   SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989)..
RN   [6]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=VSP_002588;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07200; CAA30177.1; -.
DR   EMBL; Y00051; -; NOT_ANNOTATED_CDS.
DR   EMBL; X06328; CAA29641.1; -.
DR   EMBL; X07195; CAA30173.1; -.
DR   EMBL; X07244; CAA30230.1; -.
DR   EMBL; X15051; CAA33150.1; -.
DR   EMBL; X15052; CAA33151.1; -.
DR   PIR; A29673; IJMSNL.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
FT   SIGNAL        1     19
FT   CHAIN        20   1115       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    729       POTENTIAL.
FT   DOMAIN      730   1115       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
FT   DISULFID    139    189       PROBABLE.
FT   DISULFID    235    288       PROBABLE.
FT   DISULFID    330    386       PROBABLE.
FT   DISULFID    427    480       PROBABLE.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    810   1076       Missing (in isoform N-CAM 140).
FT                                /FTId=VSP_002588.
SQ   SEQUENCE   1115 AA;  119351 MW;  2C93DCD474CFBCAF CRC64;

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 1115;
  Best Local Similarity   27.7%;  Pred. No. 1.8e-06;
  Matches   62;  Conservative   43;  Mismatches   84;  Indels   35;  Gaps   13;

Qy         26 GCMIEA-VNLKSSNR-----NPVVHEFESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
              |   || ||:|   :       |   ||:  | : |:    :|  | | ||    |:
Db        103 GTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156

Qy         79 YFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQ 136
                | :: |:  |  |      |:|  : ::|   ||||  ::|   | |::   |::||
Db        157 --DVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILA---RGEINFKDIQVIVN 209

Qy        137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSS 194
                | |      :  : |   :|:: || | :::|:|  |   || ::  |:  :   : | ::|
Db        210 VPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE-DERSRSSV 267

Qy        195 FHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                  |::  :    | |:|  :| ||| | ||      ||  ::
Db        268 ----SDSSEVTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302


RESULT 15
NCA2_XENLA
ID   NCA2_XENLA     STANDARD;      PRT;  1092 AA.
AC   P36335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93273239; PubMed=7684721;
RA   Tonissen K.F., Krieg P.A.;
RT   "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
RT   laevis are expressed during development and in adult tissues.";
RL   Gene 127:243-247(1993).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC         IsoId=P36335-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
```

```
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M76710; AAA49910.1; -.
DR   PIR; JN0635; JN0635.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 4.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19       BY SIMILARITY.
FT   CHAIN        20   1092       NEURAL CELL ADHESION MOLECULE 2, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1092       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    295       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    489       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1092 AA;  118082 MW;  CD236EE0EF8B7AD1 CRC64;

  Query Match           10.3%;  Score 169;  DB 1;  Length 1092;
  Best Local Similarity   28.4%;  Pred. No. 1.9e-06;
  Matches   59;  Conservative   33;  Mismatches   82;  Indels   34;  Gaps   11;

Qy         32 VNLKSSNR-----NPVVHEPESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
              ||||   :      |   ||   | : ||    :| |  | |: | :|      | |   :
Db        107 VNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161

Qy         85 QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIELIVQVKPVTP 142
                 |  |     |:|  : ::|   ||||  ::|   | |::   |::|| | |:
Db        162 ------RFVVLANNYLQIRGIKKTDEGNYRCEGRILA---RGEINYKDIQVIVNVPPLIQ 212

Qy        143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
               |: |   : ::  | | :::|:| |  || :   |:          :  ||  | :
Db        213 ARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDGE------EKISF--NED 263

Qy        201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                :    | |:|  :| |||:| || |
Db        264 KSEMTIYRVEKEDEAEYSCIANNQAGEA 291


Search completed: June 15, 2004, 11:03:39
Job time : 11 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 10:58:19 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1615	98.9	310	11	Q9EPK4	Q9epk4 mus musculu
2	1604	98.2	310	11	Q9D8B7	Q9d8b7 mus musculu
3	1603	98.2	310	11	Q9D1M9	Q9d1m9 mus musculu
4	1409	86.3	310	4	Q9BX67	Q9bx67 homo sapien
5	1409	86.3	355	4	Q8WWL8	Q8wwl8 homo sapien
6	1400	85.7	309	4	Q96FL1	Q96fl1 homo sapien
7	497.5	30.5	298	11	Q9JI59	Q9ji59 mus musculu
8	494.5	30.3	298	11	Q8CE95	Q8ce95 mus musculu
9	494.5	30.3	298	11	Q8C5K9	Q8c5k9 mus musculu
10	450.5	27.6	300	11	Q9JHY1	Q9jhy1 rattus norv
11	447.5	27.4	300	11	Q8VC39	Q8vc39 mus musculu
12	426	26.1	289	13	Q7ZWT0	Q7zwt0 xenopus lae
13	409.5	25.1	300	13	Q7SYQ7	Q7syq7 xenopus lae
14	340	20.8	259	4	Q9Y5B2	Q9y5b2 homo sapien
15	336	20.6	64	11	Q8BT59	Q8bt59 mus musculu
16	321	19.7	173	11	Q9JKD5	Q9jkd5 rattus norv
17	257	15.7	318	13	Q91664	Q91664 xenopus lae
18	246.5	15.1	319	11	Q922D5	Q922d5 mus musculu
19	240.5	14.7	319	11	Q9JKA5	Q9jka5 mus musculu
20	219	13.4	325	4	O95791	O95791 homo sapien
21	217.5	13.3	304	11	Q9CVA4	Q9cva4 mus musculu
22	214	13.1	335	13	Q9PWR4	Q9pwr4 gallus gall
23	213	13.0	284	4	Q9NX42	Q9nx42 homo sapien
24	213	13.0	327	4	Q96IQ7	Q96iq7 homo sapien
25	212	13.0	328	11	Q9Z109	Q9z109 mus musculu
26	209.5	12.8	335	13	Q9YGH1	Q9ygh1 gallus gall
27	208	12.7	335	13	Q9YGV5	Q9ygv5 gallus gall
28	199	12.2	181	13	Q91665	Q91665 xenopus lae
29	197.5	12.1	387	4	Q86XK7	Q86xk7 homo sapien
30	197	12.1	259	4	Q7Z2Q1	Q7z2q1 homo sapien
31	193	11.8	372	13	Q90Y50	Q90y50 brachydanio
32	192.5	11.8	407	11	Q9D2J4	Q9d2j4 mus musculu
33	190.5	11.7	248	11	Q9D0T4	Q9d0t4 mus musculu
34	185.5	11.4	795	13	Q90YM0	Q90ym0 brachydanio
35	185.5	11.4	1409	13	Q8JI27	Q8ji27 brachydanio
36	185.5	11.4	1409	13	Q801M2	Q801m2 brachydanio
37	185.5	11.4	1428	13	Q8AY67	Q8ay67 brachydanio
38	182.5	11.2	358	13	Q90490	Q90490 brachydanio
39	181	11.1	725	13	O73633	O73633 xenopus lae
40	180.5	11.1	838	13	Q90YM1	Q90ym1 brachydanio
41	179	11.0	181	11	Q9CWD9	Q9cwd9 mus musculu
42	178	10.9	416	4	Q8N7I3	Q8n7i3 homo sapien
43	177.5	10.9	298	13	Q804R4	Q804r4 brachydanio
44	177.5	10.9	1031	13	Q90YM2	Q90ym2 brachydanio
45	176.5	10.8	300	11	Q9DA22	Q9da22 mus musculu

ALIGNMENTS

RESULT 1
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

```
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   EMBL; BC024357; AAH24357.1; -.
DR   EMBL; AK032833; BAC28049.1; -.
DR   MGD; MGI:1933825; Jam3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;

  Query Match             98.9%;  Score 1615;  DB 11;  Length 310;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-152;
  Matches  308;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
Q9D8B7
ID   Q9D8B7      PRELIMINARY;      PRT;   310 AA.
AC   Q9D8B7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK008187; BAB25519.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34855 MW;  C74884EABE234680 CRC64;

  Query Match             98.2%;  Score 1604;  DB 11;  Length 310;
  Best Local Similarity   98.7%;  Pred. No. 1.4e-151;
  Matches  306;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYNWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 3
Q9D1M9
ID   Q9D1M9      PRELIMINARY;      PRT;   310 AA.
AC   Q9D1M9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003326; BAB22715.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34819 MW;  6692BCAD68EA4B1D CRC64;

  Query Match             98.2%;  Score 1603;  DB 11;  Length 310;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-151;
  Matches  305;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||:|| :|||
Db        301 DFKHKIAFVI 310


RESULT 4
Q9BX67
ID   Q9BX67      PRELIMINARY;      PRT;   310 AA.
AC   Q9BX67;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule 3 precursor (Junctional adhesion
DE   molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE   FLJ90288) (Hypothetical protein FLJ90828).
GN   JAM-2 OR JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Cunningham S.A., Arrate M.P., Tran T.M.;
RT   "Cloning of Human Junctional Adhesion Molecule 3.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT   "Heterogeneity of endothelial junctions is reflected by differential
RT   expression and specific subcellular localization of the three JAM
RT   family members.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT   "Junctional adhesion molecules (JAMs) and interendothelial
RT   junctions.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT   "Characterization of Junctional Adhesional Molecule-3 on Human
RT   Platelets: A New Member of Immunoglobulin Superfamily.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   EMBL; AF448478; AAM20925.1; -.
DR   EMBL; AK074769; BAC11195.1; -.
DR   EMBL; AK075309; BAC11538.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;

  Query Match             86.3%;  Score 1409;  DB 4;  Length 310;
  Best Local Similarity   85.8%;  Pred. No. 4.2e-132;
  Matches  266;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| |||||||||  ||| |||||||||||  |||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| |||||||:|||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:||||||||| ||::||||||||:||| |||||||| |||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
Q8WWL8
ID Q8WWL8 PRELIMINARY; PRT; 355 AA.
AC Q8WWL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within 11q24-qter for hypoplastic left
RT heart and identification of a candidate gene, JAM3, expressed during
RT cardiogenesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DBA7B1D4F8 CRC64;

Query Match 86.3%; Score 1409; DB 4; Length 355;
Best Local Similarity 85.8%; Pred. No. 5e-132;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

```
Qy          1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT 60
              ||| |  |||| |||| |||||||||:| |||||||| ||| ||||||||||||| |||
Db         46 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 105

Qy         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db        106 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 165

Qy        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        166 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 225

Qy        181 PTDSRANPRPQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
              ||||||||||:|||||:|||||||| |||||||||||||||||:|||| |:||||||
Db        226 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 285

Qy        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
              || |||||||||| |||:||:||||||||| ||::||||||||:||| |||||||| |||
Db        286 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 345

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        346 DFRHKSSFVI 355
```

RESULT 6
Q96FL1
ID Q96FL1 PRELIMINARY; PRT; 309 AA.
AC Q96FL1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010690; AAH10690.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
FT NON_TER 1 1
SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;

Query Match 85.7%; Score 1400; DB 4; Length 309;
Best Local Similarity 85.4%; Pred. No. 3.3e-131;
Matches 264; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

```
Qy          2 ALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTS 61
              || |  |||| |||| ||||||||||:| |||||||| ||| ||||||||||||| ||||
Db          1 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS 60

Qy         62 DPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALN 121
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:||||||| |
Db         61 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 120

Qy        122 DRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLP 181
              ||||:||| ||| |:||||||||:| |||||| ||| ||||||:||||||||||||||||
Db        121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 180

Qy        182 TDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLN 241
              |||||||||:||||:|||||||| ||||||||||||||||||||:|||| |:|||||||
Db        181 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240

Qy        242 IAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGD 301
              | |||||||||| |||:||:|||||||| ||::||||||||:||| |||||||| ||||
Db        241 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 300

Qy        302 FRHKSSFVI 310
              |||||||||
Db        301 FRHKSSFVI 309
```

RESULT 7
Q9JI59
ID Q9JI59 PRELIMINARY; PRT; 298 AA.
AC Q9JI59;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion
DE molecule-3) (2410030G21Rik protein).
GN JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20317114; PubMed=10779521;
RA   Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT   "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT   the Immunoglobulin Superfamily, Is Localized to Intercellular
RT   Boundaries of Endothelial Cells.";
RL   J. Biol. Chem. 275:19139-19145(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=11036763;
RA   Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT   Family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF255911; AAF81224.1; -.
DR   EMBL; AJ291757; CAC20699.1; -.
DR   EMBL; AK013914; BAB29053.1; -.
DR   EMBL; AK010616; BAB27064.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33047 MW;  1124E0F07E6CF751 CRC64;

  Query Match           30.5%;  Score 497.5;  DB 11;  Length 298;
  Best Local Similarity   37.3%;  Pred. No. 4.2e-41;
  Matches  116;  Conservative   53;  Mismatches  115;  Indels   27;  Gaps    9;

Qy         13 ARLPHPFLLLLLFRGCMIEAVNLKSSN---------RNPVVHEFESVELSCIITHSQTSDP 63
              || |   |:||    :| |::   :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDR 123
              |:||||:  |  : ||:   :|||   | ::    ::|| ||||||:  |||||  |  ::
Db         61 RLEWKKVGQG-VSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT 182
               : : |  : | | | |  | | :| :|  |    |:||: || | | | |:::    |
Db        119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy        183 DSRANPR---FQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYD 239
                ||:     |||: :|:::| | || : | |||:||| | |  |  || |: |:|
Db        175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEE 299
              |||:|||  |:||  |::|  :| | | |:| |  ||:       ||       : : |  |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF--SKETSFQKGSP-----ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
                ||:|  ||:|
Db        288 NDFKHTKSPII 298


RESULT 8
Q8CE95
ID   Q8CE95      PRELIMINARY;      PRT;   298 AA.
AC   Q8CE95;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK028757; BAC26102.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33079 MW;  CB8227EC13D349A3 CRC64;

  Query Match           30.3%;  Score 494.5;  DB 11;  Length 298;
  Best Local Similarity   37.0%;  Pred. No. 8.4e-41;
  Matches  115;  Conservative   54;  Mismatches  115;  Indels   27;  Gaps    9;

Qy         13 ARLPHPFLLLLLFRGCMIEAVNLKSSN---------RNPVVHEFESVELSCIITHSQTSDP 63
              || |   |:||    :| |::   :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDR 123
              |:||||:  |  : ||:   :|||   | ::    ::|| ||||||:  |||||  |  ::
Db         61 RLEWKKVGQG-VSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT 182
               : : |  : | | | |  | | :| :|  |    |:||: || | | | |:::    |
Db        119 GQNLQEDKVMLEVLMAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy        183 DSRANPR---FQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYD 239
                ||:     |||: :|:::| | || : | |||:||| | |  |  || |: |:|
Db        175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEE 299
              |||:|||  |:||  |::|  :| | | |:| |  ||:       ||       : : |  |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF--SKETSFQKGSP-----ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
                ||:|  ||:|
Db        288 NDFKHTKSPII 298


RESULT 9
Q8C5K9
ID   Q8C5K9      PRELIMINARY;      PRT;   298 AA.
AC   Q8C5K9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
```

```
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK078128; BAC37139.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33182 MW;  1131F0BFD89CEB51 CRC64;

  Query Match             30.3%;  Score 494.5;  DB 11;  Length 298;
  Best Local Similarity   37.3%;  Pred. No. 8.4e-41;
  Matches  116;  Conservative   53;  Mismatches  115;  Indels   27;  Gaps    9;

Qy          13 ARLPHPFLLLLLFRGCMIEAVNLKSSN---------RNPVVHEPESVELSCIITHSQTSDP 63
               || |    |:||    :| |::   :|         :   | ||:   |:|  |  :|:
Db           2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEPQEAILAC-KTPKKTTSS 60

Qy          64 RIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDR 123
               |:||||:  |  : ||:   :|||   | ::    ::|| ||||||:  ||||| |  ::
Db          61 RLEWKKVGQG-VSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy         124 -KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT 182
                : : |  : | | | |  | | :| :|  |    |:||: || | | | |:::   |
Db         119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDGHSL-- 176

Qy         183 DSRANPR---PQNSSPHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYD 239
                 ||:     |||: :|:::| | || : | |||:||| | |   |  || |: |:|
Db         177 --LGNPKGRTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy         240 LNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEE 299
               |||:|||  |:||  |::|  :| | | |:| |  ||:       ||      : : |  |
Db         235 LNISGIIATVVVVAPVISVCGLGTCYAQRKGYF--SKETSPQKGSP-----ASKVTTMSE 287

Qy         300 GDFRHKSSFVI 310
                ||:|  ||:|
Db         288 NDFKHTKSPII 298


RESULT 10
Q9JHY1
ID   Q9JHY1      PRELIMINARY;      PRT;   300 AA.
AC   Q9JHY1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule JAM.
GN   JAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley;
RA   Mashima H., Kojima I.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF276998; AAP78250.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   300 AA;  32369 MW;  45AE362A96158BFA CRC64;

  Query Match             27.6%;  Score 450.5;  DB 11;  Length 300;
  Best Local Similarity   38.0%;  Pred. No. 2.1e-36;
  Matches  114;  Conservative   52;  Mismatches  115;  Indels   19;  Gaps   10;

Qy          20 LLLLFRGCMI-EAVNLKSSNRNP----VVHEPESVELSCIITHSQTSDPRIEWKKIQDGQ 74
               || ||   ::   |  | |  :|     | | :||:| ||  :|  | ||:||| :|
Db          11 LLFLFTSMILGSLVQGKGSVYSPQTAVQVPENDSVKLPCI--YSGFSSPRVEWKFVQGST 68

Qy          75 TTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELI 134
               |  | ::|:|     | |   |  : :   :||| |:  | | :|: :  :   |::| |
Db          69 TALVCYNNQITVPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEDGGQNYGEVSIHLT 126

Qy         135 VQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT-DSRANPRPQNS 193
               | | |  |   ||::| :|  | | | | :| |   |||::: ||: | |::    | ||
Db         127 VLVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAFINS 186

Qy         194 SFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
               |: :: ::| |||: |   |||:||| | |  | | | |   ||  :||: ||:  |||
Db         187 SYTIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVT 246

Qy         253 LIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
               ||:| ::  ||  || || |  :|:      :|||   | | : |   ||:|:  |||::
Db         247 LILLGLLIFGIWFAYSRGYFERTKKG----TAPGKK--VIYSQPSARSEGEFKQTSSFLV 300


RESULT 11
Q8VC39
ID   Q8VC39      PRELIMINARY;      PRT;   300 AA.
AC   Q8VC39;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Junction cell adhesion molecule1).
GN   F11R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; BC021876; AAH21876.1; -.
DR   EMBL; AK033574; BAC28369.1; -.
DR   MGD; MGI:1321398; F11r.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
```

```
KW   Hypothetical protein.
SQ   SEQUENCE   300 AA;  32423 MW;  3CE561E8FF3B97EC CRC64;

  Query Match             27.4%;  Score 447.5;  DB 11;  Length 300;
  Best Local Similarity   34.2%;  Pred. No. 4.2e-36;
  Matches  102;  Conservative   63;  Mismatches  118;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCMIEAV-----NLKSSNRNPVVHEPESVELSCIITHSQTSDPRIEWKKIQDGQ 74
Db         11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELI 134
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT-DSRANPRFQNS 193
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LIVLAVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
Db        247 LILLGLLIFGVWFAYSRGYFERTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 12
Q7ZWT0
ID   Q7ZWT0      PRELIMINARY;      PRT;   289 AA.
AC   Q7ZWT0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to junctional adhesion molecule 1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046720; AAH46720.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   289 AA;  31630 MW;  24354B5A37618845 CRC64;

  Query Match             26.1%;  Score 426;  DB 13;  Length 289;
  Best Local Similarity   34.0%;  Pred. No. 5.6e-34;
  Matches   98;  Conservative   57;  Mismatches  113;  Indels   20;  Gaps    8;

Qy         27 CMIEAVNLKS-SNRNP--VVHEPESVELSCIITHSQTSDPRIEWKKI-QDGQTTYVYFDN 82
Db         18 CCLWTVTLAAVTTPNPTIIVKEGESAELQCSYSSDFTS-PRVEWKFVNKDQETSFVFYDG 76

Qy         83 KIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTP 142
Db         77 SLTAPYKDRAIPYPQ-GITLKQITRKDAGEYSCEVTSTGSKTLYGEAKIQLQVIVAPSKP 135

Qy        143 VCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETG 202
Db        136 VAQVPRSVSTGSVAELLCVENDGYPPPTFIWYRNKSPM----QIAP--QNSTYTIDPKTG 189

Qy        203 TLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLVVLIVLAVITMG 262
Db        190 VLKFAAVSTSDSGEYYCEATNNQGKQASDLVRMDVQDVNVGGIVAAVVIVLLILALIGFG 249

Qy        263 ICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
Db        250 MWFAYSRGYLDRKENKKVIYSLPSE--------TRSDKNFQQTSSFLV 289


RESULT 13
Q7SYQ7
ID   Q7SYQ7      PRELIMINARY;      PRT;   300 AA.
AC   Q7SYQ7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054305; AAH54305.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   300 AA;  32858 MW;  02BC49DC74E271D4 CRC64;

  Query Match             25.1%;  Score 409.5;  DB 13;  Length 300;
  Best Local Similarity   33.1%;  Pred. No. 2.6e-32;
  Matches   90;  Conservative   55;  Mismatches  104;  Indels   23;  Gaps    6;

Qy         43 VHEFESVELSCIITHSQTSD---PRIEWKKI-QDGQTTYVYFDNKIQGDLAGRTDVPGKT 98
Db         48 VKEGDSPDLRC----SYTSDYINPRVEWKFVNKDQETSFVFYDGSLTASYKDRATSYPQ- 102

Qy         99 SLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATL 158
```

```
                ::: ||| |: | ||| :   :    |  |:| | | | ||| ::|::   |  | |
Db        103 GIKLNQVTRKDAGEYSCEVTSTGTKVLYGEAKIQLQVIVAPGTPVAQVPSSARTGSVAEL 162

Qy        159 QCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYY 218
              | |::|:| | ::|| |: |:   |      |||:: ::  || | | :|   |||:||
Db        163 MCVETQGFPLPTFTWYHNNSPMQAKS------QNSTYTIDPNTGVLKFASVGTSDSGEYY 216

Qy        219 CIASNDAGAARCEGQDMEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQD 278
              | |:|  |        |:| |:|: ||:  |::||::||::  |:  || ||
Db        217 CKATNSQGEQSSAIVRMDVKDVNVGGIVAAVVIVLLILALLGFGLWFAYSRGYLDRKGNK 276

Qy        279 GESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
                | | :       |  : :|:  |||::
Db        277 KVIYSQPSE--------TRSDKNFQQTSSFLV 300


RESULT 14
Q9Y5B2
ID   Q9Y5B2      PRELIMINARY;      PRT;   259 AA.
AC   Q9Y5B2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA   Foley C., Parkos C.A.;
RT   "Human junctional adhesion molecule is expressed by polarized columnar
RT   epithelia and regulates tight junction resealing.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF154005; AAD43794.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   259 AA;  28122 MW;  FE38521A911582D0 CRC64;

  Query Match             20.8%;  Score 340;  DB 4;  Length 259;
  Best Local Similarity   30.9%;  Pred. No. 1.9e-25;
  Matches   84;  Conservative   48;  Mismatches  106;  Indels   34;  Gaps    7;

Qy         42 VVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLR 101
              :: |   |:|||   :|  | ||                :::::          |  | :
Db         19 ILPENNPVKLSC--AYSGFSSPRA------------ASYEDRV---------TFLPTGIT 55

Qy        102 IWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQ 161
              :||| |:  | | :|         |: ::||| | |   |   ||::  :|  | | |
Db         56 FKSVTREDTGTYTC-MVFEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCS 114

Qy        162 ESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIA 221
              | :| |   |:|::: : :||: ::   | |||: :|  || |||: :   |:|:| | |
Db        115 EQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEA 174

Qy        222 SNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGE 280
              |  |         ||  : |:  |:  ||| ||:| ::  ||  || || |  :|:
Db        175 RNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTS 234

Qy        281 SYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
              | |       | | : |   ||:|:  |||::
Db        235 SKK-------VIYSQPSARSEGEFKQTSSFLV 259


RESULT 15
Q8BT59
ID   Q8BT59      PRELIMINARY;      PRT;    64 AA.
AC   Q8BT59;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Junction cell adhesion molecule 3 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK017692; BAC25526.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   64 AA;  6996 MW;  AF46BC30AA6D0C11 CRC64;

  Query Match             20.6%;  Score 336;  DB 11;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-26;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        247 GGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKS 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKS 60

Qy        307 SFVI 310
              ||||
Db         61 SFVI 64


Search completed: June 15, 2004, 11:05:05
Job time : 38 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:45 ; Search time 51 Seconds
(without alignments)
1717.446 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	3	AAY96735	Aay96735 PRO1868,
2	310	100.0	310	3	AAB33457	Aab33457 Human PRO
3	310	100.0	310	3	AAB27276	Aab27276 Human con
4	310	100.0	310	4	AAB80272	Aab80272 Human PRO
5	310	100.0	310	4	AAM93905	Aam93905 Human pol
6	310	100.0	310	4	AAM93323	Aam93323 Human pol
7	310	100.0	310	4	AAU12440	Aau12440 Human PRO
8	310	100.0	310	4	AAB80383	Aab80383 Secreted
9	310	100.0	310	4	AAB80408	Aab80408 Secreted
10	310	100.0	310	4	AAB80409	Aab80409 Secreted
11	310	100.0	310	5	ABG92709	Abg92709 Human sec
12	310	100.0	310	5	ABG91361	Abg91361 Novel hum
13	310	100.0	310	5	ABB84947	Abb84947 Human PRO
14	310	100.0	310	5	ABG65297	Abg65297 Human alb
15	310	100.0	310	5	ABG65296	Abg65296 Human alb
16	310	100.0	310	5	ABG65298	Abg65298 Human alb
17	310	100.0	310	5	ABG31401	Abg31401 Human PRO
18	310	100.0	310	5	ABB95553	Abb95553 Human ang
19	310	100.0	310	6	ABU71650	Abu71650 Human PRO
20	310	100.0	310	6	ABU72377	Abu72377 Novel hum
21	310	100.0	310	6	ABU80867	Abu80867 Human sec
22	310	100.0	310	6	ABO17884	Abo17884 Novel hum
23	310	100.0	310	6	ABU71505	Abu71505 Human PRO
24	310	100.0	310	6	ADA57610	Ada57610 Human sec
25	310	100.0	310	6	ADA57611	Ada57611 Human sec
26	310	100.0	310	6	ADA57309	Ada57309 Human sec
27	310	100.0	310	6	ABP71277	Abp71277 Human jun
28	310	100.0	310	6	ABU81138	Abu81138 Human PRO
29	310	100.0	310	6	ABU71951	Abu71951 Human sec
30	310	100.0	310	6	ABO01834	Abo01834 Novel hum
31	310	100.0	310	6	ABU66838	Abu66838 Human PRO
32	310	100.0	310	6	ABU54407	Abu54407 Human sec
33	310	100.0	310	6	ABO47422	Abo47422 Human sec
34	310	100.0	310	6	ABG73314	Abg73314 Human PRO
35	310	100.0	310	6	ABU59919	Abu59919 Novel sec
36	310	100.0	310	6	ABO25109	Abo25109 Human sec
37	310	100.0	310	6	ABU64559	Abu64559 Human sec
38	310	100.0	310	6	ABU67405	Abu67405 Human sec
39	310	100.0	310	6	ABO14925	Abo14925 Human sec
40	310	100.0	310	6	ABU60813	Abu60813 Human sec
41	310	100.0	310	6	ABU67114	Abu67114 Human sec
42	310	100.0	310	6	ABU81236	Abu81236 Human PRO
43	310	100.0	310	6	ABU69682	Abu69682 Novel hum
44	310	100.0	310	6	ABO14864	Abo14864 Human sec
45	310	100.0	310	6	ADA46057	Ada46057 Novel hum

ALIGNMENTS

RESULT 1
AAY96735
ID AAY96735 standard; protein; 310 AA.
XX
AC AAY96735;
XX
DT 26-SEP-2000 (first entry)
XX
DE PRO1868, an A33 antigen homologue.
XX
KW PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .30
FT /label= Signal_peptide
FT Modified-site 26. .31
FT /note= "N-myristoylation site"
FT Modified-site 69. .77
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 104. .107
FT /note= "N-glycosylation site"
FT Modified-site 106. .109
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 107. .110
FT /note= "cAMP- and cGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 192. .195
FT /note= "N-glycosylation site"
FT Modified-site 215. .220
FT /note= "N-myristoylation site"
FT Modified-site 226. .231
FT /note= "N-myristoylation site"
FT Domain 243. .263
FT /label= Transmembrane_domain
FT Modified-site 243. .248
FT /note= "N-myristoylation site"
FT Modified-site 244. .249
FT /note= "N-myristoylation site"
FT Modified-site 262. .267
FT /note= "N-myristoylation site"
FT Modified-site 296. .299
FT /note= "Casein kinase II phosphorylation site"
XX
PN WO200036102-A2.
XX

PD 22-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US028634.
XX
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2000-431586/37.
DR N-PSDB; AAA51265.
XX
PT Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT transmembrane polypeptide.
XX
PS Claim 1; Fig 14; 154pp; English.
XX
CC This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC cancer-associated marker. The invention concerns novel secreted and
CC transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC sequences are useful in the recombinant production of PRO polypeptides,
CC as a hybridization probe to screen libraries to isolate cDNAs with
CC sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC used to produce transgenic animals useful for the development and
CC screening of therapeutically useful reagents. They can also be used in
CC gene therapy, e.g. to replace a defective gene
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 2
AAB33457

ID AAB33457 standard; protein; 310 AA.
XX
AC AAB33457;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58622.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 88; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 3
AAB27276
ID AAB27276 standard; protein; 310 AA.
XX
AC AAB27276;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #2.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA95306.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
AAB80272
ID AAB80272 standard; protein; 310 AA.
XX
AC AAB80272;
XX
DT 24-APR-2001 (first entry)

```
XX
DE   Human PRO1868 protein.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
PF   22-FEB-2000; 2000WO-US004414.
XX
PR   07-JUL-1999;   99US-0143048P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N;
PI   Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen MB,  Goddard A;
PI   Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ,  Kljavin IJ;
PI   Mather JP,  Pan J,  Paoni NF,  Roy MA,  Stewart TA,  Tumas D;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-081051/09.
DR   N-PSDB; AAF72433.
XX
PT   Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT   treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT   cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT   disease).
XX
PS   Claim 1; Fig 124; 393pp; English.
XX
CC   The present sequence is one of sixty one novel secreted and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful for treating skin
CC   diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC   gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC   diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC   cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC   ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC   disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC   infertility, AIDS and diabetes and retinal disorders such as retinitis
CC   pigmentosum. The PRO nucleic acids have applications in molecular
CC   biology, including use as hybridization probes, and in chromosome and
CC   gene mapping
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 5
AAM93905
ID   AAM93905 standard; protein; 310 AA.
XX
AC   AAM93905;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 4051.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94867.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
```

```
XX
SQ   Sequence 310 AA;

  Query Match            100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
AAM93323
ID   AAM93323 standard; protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94243.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match            100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
AAU12440
ID   AAU12440 standard; protein; 310 AA.
XX
AC   AAU12440;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO1868 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PP   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
```

```
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21512.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 12; Fig 538; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 8
AAB80383
ID   AAB80383 standard; protein; 310 AA.
XX
AC   AAB80383;
XX
DT   24-APR-2001  (first entry)
XX
DE   Secreted protein encoded by gene #13.
XX
KW   Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW   cerebrovascular; infection; food.
XX
OS   Homo sapiens.
XX
PN   WO200107459-A1.
XX
PD   01-FEB-2001.
XX
PF   20-JUL-2000; 2000WO-US019735.
XX
PR   23-JUL-1999;   99US-0145220P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI   Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR   WPI; 2001-123261/13.
XX
PT   New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT   preventing and treating e.g. autoimmune, hyperproliferative,
PT   cardiovascular, and ocular diseases or disorders and microorganism
PT   infections.
XX
PS   Claim 11; Page 538-539; 601pp; English.
XX
CC   The present invention relates to 29 human secreted proteins. The
CC   invention is used to prevent autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. Also used in food
CC   preparations
XX
SQ   Sequence 310 AA;
```

```
  Query Match          100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 9
AAB80408
ID AAB80408 standard; protein; 310 AA.
XX
AC AAB80408;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #38.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

```
  Query Match          100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 10
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or

```
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. Also used in food
CC   preparations
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 11
ABG92709
ID   ABG92709 standard; protein; 310 AA.
XX
AC   ABG92709;
XX
DT   18-NOV-2002  (first entry)
XX
DE   Human secreted protein PRO1868.
XX
KW   Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW   PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW   inflammatory disorder; immune related disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW   autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW   psoriasis; allergic disease of the lung; graft-versus host disease;
KW   tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002098506-A1.
XX
PD   25-JUL-2002.
XX
PF   27-DEC-2001; 2001US-00033301.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-690475/74.
DR   N-PSDB; ABS68392.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides useful
PT   for diagnosis and treatment of inflammatory disorders and immune-related
PT   diseases, and identifying modulators.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to an isolated polypeptide having at least 80%
CC   amino acid sequence identity to secreted and transmembrane polypeptides
CC   PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC   PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC   cells and antibodies against PRO polypeptides. PRO proteins are useful
CC   for identifying modulators of the polypeptide. PRO1868 useful for the
CC   diagnosis and treatment of inflammatory and immune related diseases
CC   including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC   sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC   infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC   versus host disease and tumours. Pro nucleic acids are useful for
CC   constructing hybridisation probes for mapping the gene that encodes that
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   and for generating transgenic animals which are useful in the development
CC   and screening of therapeutically useful reagents. PRO nucleic acids are
CC   also useful for gene therapy, chromosome identification, and tissue
CC   typing. PRO proteins are useful as molecular weight markers for protein
CC   electrophoresis purposes. The anti-PRO antibodies are useful in
CC   diagnostic assays for PRO, e.g. detecting its expression in specific
CC   cells, tissues or serum and for affinity purification of PRO. The present
CC   sequence represents a PRO protein
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 12
ABG91361
ID   ABG91361 standard; protein; 310 AA.
XX
AC   ABG91361;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Novel human secreted protein #7.
XX
KW   Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW   immunogenic.
XX
OS   Homo sapiens.
XX
PN   US2002098505-A1.
XX
PD   25-JUL-2002.
XX
PF   28-DEC-2001; 2001US-00033246.
XX
PR   04-AUG-1998;   98US-0095325P.
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
PR   29-OCT-1999;   99US-0162506P.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   09-DEC-1999;   99US-0170262P.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-665999/71.
DR   N-PSDB; ABS67460.
XX
PT   New human secreted and transmembrane (PRO) polypeptides, useful for
PT   treating conditions requiring PRO polypeptides, for screening PRO
PT   antagonists and agonists useful as drug candidates.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to new human secreted and transmembrane proteins
CC   (PRO) and nucleic acids of the invention. The polypeptides can be
CC   administered therapeutically, especially by expressing encoding
CC   polynucleotides, e.g. in therapeutic compositions. They can be used to
CC   screen for PRO polypeptide antagonists and agonists useful to identify
CC   drug candidates. They can also be used to produce antibodies, useful to
CC   detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC   therapeutically (e.g. as antagonists or to target and/or deliver
CC   cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC   produce antisense sequences to inhibit polypeptide production. They can
CC   be used to produce probes and primers useful to detect or isolate
CC   sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC   sequences from other species. They are also useful for gene mapping and
CC   to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC   amino acid sequences of the invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
ABB84947
ID   ABB84947 standard; protein; 310 AA.
XX
AC   ABB84947;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO1868 protein sequence SEQ ID NO:262.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US019692.
XX
PR   23-JUN-2000; 2000US-0213637P.
```

PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88202.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 262; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy 61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy 121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy 241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy 301 DFRHKSSFVI 310
||||||||||
Db 301 DFRHKSSFVI 310

RESULT 14
ABG65297
ID ABG65297 standard; protein; 310 AA.
XX
AC ABG65297;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human albumin fusion protein #1972.
XX
KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177137-A1.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011988.
XX
PR 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
PR 21-DEC-2000; 2000US-0256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Haseltine WA;
XX
DR WPI; 2002-010886/01.
XX
PT New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
PS Claim 1; Page 1895; 2102pp; English.
XX
CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's

```
CC   disease, ulcerative colitis), immune disorders (e.g. acquired
CC   immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC   haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC   Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC   schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC   ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
ABG65296
ID   ABG65296 standard; protein; 310 AA.
XX
AC   ABG65296;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human albumin fusion protein #1971.
XX
KW   Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW   human serum albumin; HSA; cancer; reproductive disorder;
KW   digestive disorder; immune disorder; endocrine disorder;
KW   haematopoietic disorder; neural disorder; connective disorder;
KW   cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW   immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW   neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW   osteopathic; antiarthritic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177137-A1.
XX
PD   18-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011988.
XX
PR   12-APR-2000; 2000US-0229358P.
PR   25-APR-2000; 2000US-0199384P.
PR   21-DEC-2000; 2000US-0256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2002-010886/01.
XX
PT   New fusion protein for treating disease e.g. diabetes comprises an
PT   albumin fused to a therapeutic protein.
XX
PS   Claim 1; Page 1893-1894; 2102pp; English.
XX
CC   The present invention relates to albumin fusion proteins comprising a
CC   therapeutic protein X and human albumin (HA, also known as human serum
CC   albumin, HSA). The proteins are useful for treating a disease or disorder
CC   that may be modulated by therapeutic protein X. The albumin extends the
CC   shelf-life of protein X, and may increase its biological in vitro/in vivo
CC   activity. The protein is useful for treating and diagnosing disorders
CC   such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC   disease, ulcerative colitis), immune disorders (e.g. acquired
CC   immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC   haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC   Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC   schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC   ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 310;  DB 5;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: June 15, 2004, 11:09:57
Job time : 52 secs
```

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:08:05 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	4	US-09-907-794A-423	Sequence 423, App
2	310	100.0	310	4	US-09-905-125A-423	Sequence 423, App
3	310	100.0	310	4	US-09-902-775A-423	Sequence 423, App
4	7	2.3	14	2	US-08-310-912A-190	Sequence 190, App
5	7	2.3	14	3	US-09-301-085-190	Sequence 190, App
6	7	2.3	14	5	PCT-US95-04589-190	Sequence 190, App
7	7	2.3	52	3	US-09-330-330-9	Sequence 9, Appli
8	7	2.3	119	4	US-09-134-001C-5228	Sequence 5228, Ap
9	7	2.3	148	4	US-09-489-039A-14211	Sequence 14211, A
10	7	2.3	215	4	US-09-328-352-6750	Sequence 6750, Ap
11	7	2.3	220	4	US-09-134-000C-6778	Sequence 6778, Ap
12	7	2.3	223	4	US-09-252-991A-32267	Sequence 32267, A
13	7	2.3	224	4	US-09-252-991A-24969	Sequence 24969, A
14	7	2.3	240	4	US-09-252-991A-17237	Sequence 17237, A
15	7	2.3	241	1	US-08-484-272-2	Sequence 2, Appli
16	7	2.3	241	1	US-08-476-489-2	Sequence 2, Appli
17	7	2.3	241	1	US-08-467-070-2	Sequence 2, Appli
18	7	2.3	241	1	US-08-467-070A-2	Sequence 2, Appli
19	7	2.3	241	5	PCT-US93-11669-2	Sequence 2, Appli
20	7	2.3	244	3	US-08-883-086-9	Sequence 9, Appli
21	7	2.3	244	4	US-09-589-287B-5	Sequence 5, Appli
22	7	2.3	244	4	US-09-588-947A-5	Sequence 5, Appli
23	7	2.3	244	4	US-09-131-237C-5	Sequence 5, Appli
24	7	2.3	244	4	US-09-589-286A-5	Sequence 5, Appli
25	7	2.3	249	2	US-09-154-802-1	Sequence 1, Appli
26	7	2.3	249	3	US-09-373-029-1	Sequence 1, Appli
27	7	2.3	325	4	US-09-252-991A-31408	Sequence 31408, A
28	7	2.3	333	1	US-08-148-215A-4	Sequence 4, Appli
29	7	2.3	333	4	US-09-170-496D-16	Sequence 16, Appl
30	7	2.3	333	4	US-09-170-496D-172	Sequence 172, App
31	7	2.3	454	4	US-09-240-639-11	Sequence 11, Appl
32	7	2.3	494	4	US-09-252-991A-28162	Sequence 28162, A
33	7	2.3	503	4	US-09-215-694-8	Sequence 8, Appli
34	7	2.3	517	4	US-09-252-991A-19322	Sequence 19322, A
35	7	2.3	524	2	US-08-928-692-12	Sequence 12, Appl
36	7	2.3	524	4	US-09-339-972-12	Sequence 12, Appl
37	7	2.3	547	4	US-09-252-991A-18576	Sequence 18576, A
38	7	2.3	556	4	US-09-252-991A-18110	Sequence 18110, A
39	7	2.3	603	4	US-09-252-991A-25264	Sequence 25264, A
40	7	2.3	621	4	US-09-252-991A-19749	Sequence 19749, A
41	7	2.3	642	1	US-08-706-936-2	Sequence 2, Appli
42	7	2.3	642	1	US-08-706-936-3	Sequence 3, Appli
43	7	2.3	643	2	US-08-616-844-39	Sequence 39, Appl
44	7	2.3	643	2	US-08-599-654-39	Sequence 39, Appl
45	7	2.3	643	3	US-08-944-868A-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
```

```
Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 3
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Pilvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-775A-423

  Query Match           100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-279;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 4
US-08-310-912A-190
; Sequence 190, Application US/08310912A
; Patent No. 5981730
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  208
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2904
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,912A
;      FILING DATE:  September 22, 1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/227,360
;      FILING DATE:  April 13, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/254001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  190:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-310-912A-190

  Query Match             2.3%;  Score 7;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 LALITLG 262
              |||||||
Db          5 LALITLG 11


RESULT 5
US-09-301-085-190
; Sequence 190, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
;  APPLICANT: Ausubel, Frederick M.
;  APPLICANT: Staskawicz, Brian J.
;  APPLICANT: Brent, Andrew F.
;  APPLICANT: Dahlbeck, Douglas
;  APPLICANT: Katagiri, Fumiaki
;  APPLICANT: Kunkel, Barbara N.
;  APPLICANT: Mindrinos, Michael N.
;  APPLICANT: Yu, Guo-Liang
;  TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
;  TITLE OF INVENTION: DETECTION  METHODS
;  FILE REFERENCE: 00786/254002
;  CURRENT APPLICATION NUMBER: US/09/301,085
;  CURRENT FILING DATE: 1999-04-28
;  EARLIER APPLICATION NUMBER: 08/310,912
;  EARLIER FILING DATE: 1994-09-22
;  EARLIER APPLICATION NUMBER: 08/227,360
;  EARLIER FILING DATE: 1994-04-13
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-301-085-190

  Query Match             2.3%;  Score 7;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 LALITLG 262
              |||||||
Db          5 LALITLG 11


RESULT 6
```

```
PCT-US95-04589-190
; Sequence 190, Application PC/TUS9504589
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE AND USES THEREOF
;    NUMBER OF SEQUENCES:  201
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2904
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04589
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,360
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/230001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  190:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-04589-190

  Query Match             2.3%;  Score 7;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 LALITLG 262
              |||||||
Db          5 LALITLG 11


RESULT 7
US-09-330-330-9
; Sequence 9, Application US/09330330
; Patent No. 6274789
;  GENERAL INFORMATION:
;    APPLICANT:  Yano, Masahiro
;    APPLICANT:  Iwamoto, Masao
;    APPLICANT:  Katayose, Yuichi
;    APPLICANT:  Sasaki, Takuji
;    APPLICANT:  Wang, Zi-Xuan
;    APPLICANT:  Yamanouchi, Utako
;    APPLICANT:  Ishimaru, Lisa
;    TITLE OF INVENTION:  RICE GENE RESISTANT TO BLAST DISEASE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
```

```
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/330,330
;      FILING DATE:  11-JUN-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 10-181455
;      FILING DATE:  12-JUN-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Ph.D., J.D., Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  06501/032001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-330-330-9

  Query Match             2.3%;  Score 7;  DB 3;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 LALITLG 262
              |||||||
Db         37 LALITLG 43


RESULT 8
US-09-134-001C-5228
; Sequence 5228, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5228
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5228

  Query Match             2.3%;  Score 7;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        251 VVLAVLA 257
              |||||||
Db         48 VVLAVLA 54


RESULT 9
US-09-489-039A-14211
; Sequence 14211, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 14211
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14211

  Query Match             2.3%;  Score 7;  DB 4;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        253 LAVLALI 259
              |||||||
Db         89 LAVLALI 95


RESULT 10
US-09-328-352-6750
; Sequence 6750, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6750
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-6750

  Query Match             2.3%;  Score 7;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        243 GGIIGGV 249
              |||||||
Db        100 GGIIGGV 106


RESULT 11
US-09-134-000C-6778
; Sequence 6778, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6778
;   LENGTH: 220
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
```

US-09-134-000C-6778

Query Match 2.3%; Score 7; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        243 GGIIGGV 249
              |||||||
Db         50 GGIIGGV 56
```

RESULT 12
US-09-252-991A-32267
; Sequence 32267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32267
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32267

Query Match 2.3%; Score 7; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 RRPPRLR 10
              |||||||
Db          5 RRPPRLR 11
```

RESULT 13
US-09-252-991A-24969
; Sequence 24969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24969
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24969

Query Match 2.3%; Score 7; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 RRPPRLR 10
              |||||||
Db         44 RRPPRLR 50
```

RESULT 14
US-09-252-991A-17237
; Sequence 17237, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17237
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17237

Query Match 2.3%; Score 7; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 RRPPRLR 10
              |||||||
Db        191 RRPPRLR 197
```

RESULT 15
US-08-484-272-2
; Sequence 2, Application US/08484272
; Patent No. 5661004
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: WARE, Carl
; TITLE OF INVENTION: LYMPHOTOXIN-BETA, LYMPHOTOXIN-BETA
; TITLE OF INVENTION: COMPLEXES, PHARMACEUTICAL PREPARATIONS AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,272
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,614
; FILING DATE:
; APPLICATION NUMBER: PCT/US91/04588
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/544,862
; FILING DATE: 27-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B129CIPII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090

; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-272-2

Query Match 2.3%; Score 7; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        252 VLAVLAL 258
              |||||||
Db         37 VLAVLAL 43
```

Search completed: June 15, 2004, 11:13:23
Job time : 17.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:10:00 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1158786 seqs, 281726120 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	9	US-09-909-320-423	Sequence 423, App
2	310	100.0	310	9	US-09-909-088B-423	Sequence 423, App
3	310	100.0	310	9	US-09-905-291A-423	Sequence 423, App
4	310	100.0	310	9	US-09-902-853-423	Sequence 423, App
5	310	100.0	310	9	US-09-907-824-423	Sequence 423, App
6	310	100.0	310	9	US-09-907-841-423	Sequence 423, App
7	310	100.0	310	10	US-09-904-011-423	Sequence 423, App
8	310	100.0	310	10	US-09-906-742-423	Sequence 423, App
9	310	100.0	310	10	US-09-906-838-423	Sequence 423, App
10	310	100.0	310	10	US-09-907-613-423	Sequence 423, App
11	310	100.0	310	10	US-09-907-942-423	Sequence 423, App
12	310	100.0	310	10	US-09-904-859-423	Sequence 423, App
13	310	100.0	310	10	US-09-909-204-423	Sequence 423, App
14	310	100.0	310	10	US-09-904-820-423	Sequence 423, App
15	310	100.0	310	10	US-09-904-786-423	Sequence 423, App
16	310	100.0	310	10	US-09-906-646-423	Sequence 423, App
17	310	100.0	310	10	US-09-906-700-423	Sequence 423, App
18	310	100.0	310	10	US-09-903-786-423	Sequence 423, App
19	310	100.0	310	10	US-09-902-903-423	Sequence 423, App
20	310	100.0	310	10	US-09-903-749A-423	Sequence 423, App
21	310	100.0	310	10	US-09-904-119-423	Sequence 423, App
22	310	100.0	310	10	US-09-904-956-423	Sequence 423, App
23	310	100.0	310	10	US-09-902-736-423	Sequence 423, App
24	310	100.0	310	10	US-09-907-794-423	Sequence 423, App
25	310	100.0	310	10	US-09-903-943-423	Sequence 423, App
26	310	100.0	310	10	US-09-904-462-423	Sequence 423, App
27	310	100.0	310	10	US-09-907-925-423	Sequence 423, App
28	310	100.0	310	10	US-09-902-692-423	Sequence 423, App
29	310	100.0	310	10	US-09-903-520-423	Sequence 423, App
30	310	100.0	310	10	US-09-905-056-423	Sequence 423, App
31	310	100.0	310	10	US-09-909-064-423	Sequence 423, App
32	310	100.0	310	10	US-09-904-553-423	Sequence 423, App
33	310	100.0	310	10	US-09-905-381-423	Sequence 423, App
34	310	100.0	310	10	US-09-905-088-423	Sequence 423, App
35	310	100.0	310	10	US-09-907-575-423	Sequence 423, App
36	310	100.0	310	10	US-09-905-075-423	Sequence 423, App
37	310	100.0	310	10	US-09-902-759-423	Sequence 423, App
38	310	100.0	310	10	US-09-902-634-423	Sequence 423, App
39	310	100.0	310	10	US-09-902-713-423	Sequence 423, App
40	310	100.0	310	10	US-09-907-979-423	Sequence 423, App
41	310	100.0	310	10	US-09-902-615-423	Sequence 423, App
42	310	100.0	310	10	US-09-903-925-423	Sequence 423, App
43	310	100.0	310	10	US-09-906-760A-423	Sequence 423, App
44	310	100.0	310	10	US-09-903-823-423	Sequence 423, App
45	310	100.0	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

```
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-320-423

  Query Match             100.0%;  Score 310;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,088B
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-088B-423

  Query Match             100.0%;  Score 310;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 3
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,291A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-291A-423

  Query Match            100.0%;  Score 310;  DB 9;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-423

Query Match 100.0%; Score 310; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

```
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-824-423

  Query Match             100.0%;  Score 310;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,841
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-841-423

  Query Match             100.0%;  Score 310;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011
```

```
; Publication No. US20030003530A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,011
;  CURRENT FILING DATE:  2001-07-11
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
```

```
US-09-904-011-423

  Query Match           100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 8
US-09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,742
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
```

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 9
US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 10
US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,613
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-613-423

  Query Match           100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 11
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

```
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-859-423

  Query Match             100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,204
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-204-423

  Query Match             100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 14
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,820
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-820-423

  Query Match             100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
US-09-904-786-423
; Sequence 423, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
```

```
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,786
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-786-423

  Query Match             100.0%;  Score 310;  DB 10;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-293;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: June 15, 2004, 11:14:53
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:06:35 ; Search time 14 Seconds
(without alignments)
2129.955 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	290	2	I68750	MHC class I lympho
2	8	2.6	336	2	A86406	probable RING zinc
3	8	2.6	342	1	HLHUC4	MHC class I histoc
4	8	2.6	348	2	E82933	type I restriction
5	8	2.6	366	2	JH0546	class I histocompa
6	8	2.6	366	2	JH0547	class I histocompa
7	8	2.6	366	2	JH0545	class I histocompa
8	8	2.6	366	2	I37078	HLA-C alpha chain
9	8	2.6	492	2	AB1013	probable membrane
10	8	2.6	784	2	A86676	carbon starvation
11	7	2.3	77	2	JC5645	lymphotoxin beta -
12	7	2.3	113	2	AH1748	hypothetical prote
13	7	2.3	171	2	G70548	hypothetical prote
14	7	2.3	172	2	T08548	hypothetical prote
15	7	2.3	173	2	T01282	hypothetical prote
16	7	2.3	173	2	B90241	hypothetical prote
17	7	2.3	173	2	T25730	hypothetical prote
18	7	2.3	177	2	E85833	partial probable s
19	7	2.3	177	2	B90988	partial probable s
20	7	2.3	208	2	T03627	GTP-binding protei
21	7	2.3	208	2	T01588	GTP-binding protei
22	7	2.3	211	2	E86888	hypothetical prote
23	7	2.3	214	2	T47268	phosphatidylserine
24	7	2.3	217	2	T30446	occlusion-derived
25	7	2.3	242	2	G84315	cobalt transport p
26	7	2.3	244	2	A46066	lymphotoxin beta -
27	7	2.3	255	2	T35883	transcription regu
28	7	2.3	280	2	PH0269	epidermal autoanti
29	7	2.3	294	2	H84023	phosphate ABC tran
30	7	2.3	297	2	AB3037	hypothetical prote
31	7	2.3	297	2	A81002	conserved hypothet
32	7	2.3	299	2	A98249	nitrate transport
33	7	2.3	300	2	A82017	probable lipoprote
34	7	2.3	302	2	B70471	heat shock protein
35	7	2.3	306	2	I49139	lymphotoxin-beta -
36	7	2.3	314	2	AG3093	hypothetical prote
37	7	2.3	314	2	C98193	sugar transport sy
38	7	2.3	324	2	T27302	hypothetical prote
39	7	2.3	333	2	I38974	G protein-coupled
40	7	2.3	343	2	H95879	probable sugar ABC
41	7	2.3	346	2	D75303	conserved hypothet
42	7	2.3	362	2	G75614	GGDEF family prote
43	7	2.3	375	2	T46378	hypothetical prote
44	7	2.3	376	2	F71815	hypothetical prote
45	7	2.3	380	2	E88421	protein R74.2 [imp

ALIGNMENTS

RESULT 1
I68750
MHC class I lymphocyte antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C;Accession: I68750
R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B
A;Reference number: I54457; MUID:89233295; PMID:2714852
A;Accession: I68750
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-290 <RES>
A;Cross-references: GB:M28207; NID:g576478; PIDN:AAA53259.1; PID:g576479
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;144-209/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
||||||||
Db 241 VLVVLAVL 248

RESULT 2
A86406
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86406
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <STO>
A;Cross-references: GB:AE005172; NID:g11024872; PIDN:AAG26956.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 2.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        250 LVVLAVLA 257
              ||||||||
Db         28 LVVLAVLA 35
```

RESULT 3
HLHUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C;Accession: A24512
R;Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A;Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A;Reference number: A92500; MUID:86033791; PMID:3863816
A;Accession: A24512
A;Molecule type: DNA
A;Residues: 1-342 <DAV>
A;Cross-references: GB:M11886; NID:g184173; PIDN:AAA52665.1; PID:g386777
C;Genetics:
A;Gene: GDB:HLA-C
A;Cross-references: GDB:119311; OMIM:142840
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology <IMM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        249 VLVVLAVL 256
              ||||||||
Db        293 VLVVLAVL 300
```

RESULT 4
E82933
type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma ure
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002
C;Accession: E82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A;Reference number: A82870
A;Accession: E82933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30504.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: hsdM-1; UU098
A;Genetic code: SGC3
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 2.6%; Score 8; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        123 RKEIDEIV 130
              ||||||||
Db        336 RKEIDEIV 343
```

RESULT 5
JH0546
class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0546
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Reference number: JH0534; MUID:92078860; PMID:1744581
A;Accession: JH0546
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60249; NID:g22882; PIDN:CAA42801.1; PID:g22883
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status pr
F;25-114/Domain: alpha-1 <AL1>
F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324
```

RESULT 6
JH0547
class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0547
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Reference number: JH0534; MUID:92078860; PMID:1744581
A;Accession: JH0547
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60248; NID:g22884; PIDN:CAA42800.1; PID:g22885
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0203 #status pr
F;25-114/Domain: alpha-1 <AL1>
F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324
```

RESULT 7
JH0545
class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla

C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0545
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A;Reference number: JH0534; MUID:92078860; PMID:1744581
A;Accession: JH0545
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60251; NID:g22880; PIDN:CAA42803.1; PID:g22881
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre
F;25-114/Domain: alpha-1 <AL1>
F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-366/Domain: intracellular #status predicted <INT>

  Query Match 2.6%; Score 8; DB 2; Length 366;
  Best Local Similarity 100.0%; Pred. No. 7.1;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
 ||||||||
Db 317 VLVVLAVL 324

RESULT 8
I37078
HLA-C alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37078
R;Vilches, C.; Bunce, M.; de pablo, R.; Herrero, M.J.; Kreisler, M.
Tissue Antigens 46, 19-23, 1995
A;Title: Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by PCR-SSP.
A;Reference number: I37078; MUID:96086482; PMID:7482492
A;Accession: I37078
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-366 <RES>
A;Cross-references: EMBL:X83394; NID:g669131; PIDN:CAA58313.1; PID:g669132
C;Genetics:
A;Gene: Cw*0704
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match 2.6%; Score 8; DB 2; Length 366;
  Best Local Similarity 100.0%; Pred. No. 7.1;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
 ||||||||
Db 317 VLVVLAVL 324

RESULT 9
AB1013
probable membrane protein STY4415 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB1013
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB1013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09203.1; PID:g16505207; GSPDB:GN00176
C;Genetics:
A;Gene: STY4415

  Query Match 2.6%; Score 8; DB 2; Length 492;
  Best Local Similarity 100.0%; Pred. No. 9.2;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IGGIIGGV 249
 ||||||||
Db 244 IGGIIGGV 251

RESULT 10
A86676
carbon starvation protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: A86676
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STO>
A;Cross-references: GB:AE005176; PID:g12723283; PIDN:AAK04507.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: cstA
C;Superfamily: carbon starvation protein

  Query Match 2.6%; Score 8; DB 2; Length 784;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLAVLALI 259
 ||||||||
Db 223 VLAVLALI 230

RESULT 11
JC5645
lymphotoxin beta - human
N;Alternate names: non-Hodgkin's lymphoma
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 05-Nov-1999
C;Accession: JC5645
R;Warzocha, K.; Renard, N.; Charlot, C.; Bienvenu, J.; Coiffier, B.; Salles, G.
Biochem. Biophys. Res. Commun. 238, 273-276, 1997
A;Title: Identification of two lymphotoxin beta isoforms expressed in human lymphoid ce
A;Reference number: JC5645; MUID:97445965; PMID:9299492
A;Accession: JC5645
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-77 <WAR>
A;Cross-references: GB:U89922; NID:g1870795; PIDN:AAC51769.1; PID:g1870796
C;Comment: This protein is involved in the development and function of the immune syste

  Query Match 2.3%; Score 7; DB 2; Length 77;
  Best Local Similarity 100.0%; Pred. No. 19;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLAVLAL 258
 |||||||

```
Db         40 VLAVLAL 46


RESULT 12
AH1748
hypothetical protein lin2533 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH1748
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97760.1; PID:g16415055; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2533

  Query Match             2.3%;  Score 7;  DB 2;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        243 GGIIGGV 249
              |||||||
Db         15 GGIIGGV 21


RESULT 13
G70548
hypothetical protein Rv0556 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C;Accession: G70548
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70548
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-171 <COL>
A;Cross-references: GB:Z95558; GB:AL123456; NID:g3261781; PIDN:CAB08967.1; PID:e316801;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0556
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0556

  Query Match             2.3%;  Score 7;  DB 2;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 LVVLAVL 256
              |||||||
Db        150 LVVLAVL 156


RESULT 14
T08548
hypothetical protein F27B13.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T08548
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; M
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16442
A;Accession: T08548
A;Molecule type: DNA
A;Residues: 1-172 <BEV>
A;Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.110
A;Experimental source: cultivar Columbia; BAC clone F27B13
C;Genetics:
A;Gene: ATSP:F27B13.110
A;Map position: 4

  Query Match             2.3%;  Score 7;  DB 2;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 RPPRLRL 11
              |||||||
Db         37 RPPRLRL 43


RESULT 15
T01282
hypothetical protein At2g19340 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F27F23.14
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01282; E84575
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Ka
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
A;Reference number: Z14177
A;Accession: T01282
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-173 <ROU>
A;Cross-references: EMBL:AC003058; NID:g3135250; PID:g3135264
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: GB:AE002093; NID:g3135264; PIDN:AAC16464.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g19340; F27F23.14
A;Map position: 2

  Query Match             2.3%;  Score 7;  DB 2;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 RPPRLRL 11
              |||||||
Db         38 RPPRLRL 44


Search completed: June 15, 2004, 11:12:37
Job time : 15 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:10 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	80	1	TX3A_PHONI	P81793 phoneutria
2	8	2.6	366	1	1C02_GORGO	P30385 gorilla gor
3	8	2.6	366	1	1C03_GORGO	P30386 gorilla gor
4	8	2.6	366	1	1C04_GORGO	P30387 gorilla gor
5	8	2.6	366	1	1C07_HUMAN	P10321 homo sapien
6	8	2.6	366	1	1C18_HUMAN	Q29865 homo sapien
7	8	2.6	435	1	YGIK_SALTY	P40800 salmonella
8	7	2.3	161	1	TATB_STRCO	Q9fbk8 streptomyce
9	7	2.3	224	1	XLR1_MOUSE	Q9z114 mus musculu
10	7	2.3	242	1	RS2_SHEON	Q8egh5 shewanella
11	7	2.3	244	1	TNFC_HUMAN	Q06643 homo sapien
12	7	2.3	244	1	TNFC_PANTR	Q862z7 pan troglod
13	7	2.3	302	1	HTPX_AQUAE	O67798 aquifex aeo
14	7	2.3	306	1	TNFC_MOUSE	P41155 mus musculu
15	7	2.3	310	1	TNFC_MARMO	Q9jm10 marmota mon
16	7	2.3	333	1	GPR8_HUMAN	P48146 homo sapien
17	7	2.3	343	1	HMD_METVO	Q50840 methanococc
18	7	2.3	374	1	TRM1_SULTO	Q971v9 sulfolobus
19	7	2.3	403	1	TYRP_ECOLI	P18199 escherichia
20	7	2.3	417	1	PVR_CERAE	P32506 cercopithec
21	7	2.3	417	1	PVR_HUMAN	P15151 homo sapien
22	7	2.3	418	1	SYTF_MOUSE	Q8c6n3 mus musculu
23	7	2.3	454	1	APY_SOLTU	P80595 solanum tub
24	7	2.3	481	1	LMRA_STRLN	P46104 streptomyce
25	7	2.3	491	1	CPB4_RABIT	P00178 oryctolagus
26	7	2.3	491	1	CPB5_RABIT	P12789 oryctolagus
27	7	2.3	524	1	GTR2_HUMAN	P11168 homo sapien
28	7	2.3	574	1	IRL2_MOUSE	Q9ers7 mus musculu
29	7	2.3	595	1	IF2P_ARCFU	O29490 archaeoglob
30	7	2.3	617	1	PYS1_PSEAE	Q06583 pseudomonas
31	7	2.3	643	1	S212_HUMAN	Q92959 homo sapien
32	7	2.3	643	1	S212_MOUSE	Q9ept5 mus musculu
33	7	2.3	643	1	S212_RAT	Q00910 rattus norv
34	7	2.3	688	1	PYS2_PSEAE	Q06584 pseudomonas
35	7	2.3	693	1	NCPR_ASPNG	Q00141 aspergillus
36	7	2.3	697	1	TGM2_CHICK	Q01841 gallus gall
37	7	2.3	721	1	YJIY_ECOLI	P39396 escherichia
38	7	2.3	729	1	GOA5_MOUSE	Q9qye6 mus musculu
39	7	2.3	758	1	SC18_YEAST	P18759 saccharomyc
40	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
41	7	2.3	909	1	RPS2_ARATH	Q42484 arabidopsis
42	7	2.3	981	1	SCA4_RICPE	Q9aj37 rickettsia
43	7	2.3	987	1	K6P1_CANAL	O94201 candida alb
44	7	2.3	991	1	SCA4_RICSI	Q9aj77 rickettsia
45	7	2.3	1011	1	SCA4_RICAF	Q9aj83 rickettsia

ALIGNMENTS

RESULT 1
TX3A_PHONI
ID TX3A_PHONI STANDARD; PRT; 80 AA.
AC P81793;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin Pn3A precursor.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99053416; PubMed=9839681;
RA Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.P.,
RA Cordeiro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,
RA Gomez M.V., Beirao P.S.L.;
RT "Cloning, cDNA sequence analysis and patch clamp studies of a toxin
RT from the venom of the armed spider (Phoneutria nigriventer).";
RL Toxicon 36:1971-1980(1998).
CC -!- FUNCTION: Antagonist of L-type calcium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the spider toxin Tx3 family.
DR InterPro; IPR004169; spidertoxin.
DR Pfam; PF02819; spidertoxin; 1.
KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 37 BY SIMILARITY.
FT CHAIN 38 71 NEUROTOXIN PN3A.
FT PROPEP 72 80 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8937 MW; B5BF209257EB6793 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 LALITLGI 263
||||||||
Db 12 LALITLGI 19

RESULT 2
1C02_GORGO
ID 1C02_GORGO STANDARD; PRT; 366 AA.
AC P30385;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Class I histocompatibility antigen, GOGO-C0201 alpha chain precursor.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

```
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60251; CAA42803.1; -.
DR   PIR; JH0545; JH0545.
DR   HSSP; P30685; 1A9E.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    366       CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 GOGO-C0201 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    333
FT   DOMAIN      334    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   366 AA;  40954 MW;  05E159364C769FC5 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324


RESULT 3
1C03_GORGO
ID   1C03_GORGO     STANDARD;      PRT;   366 AA.
AC   P30386;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-APR-1993 (Rel. 25, Last annotation update)
DE   Class I histocompatibility antigen, GOGO-C0202 alpha chain precursor.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60249; CAA42801.1; -.
DR   PIR; JH0546; JH0546.
DR   HSSP; P03989; 1HSA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    366       CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 GOGO-C0202 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    332
FT   DOMAIN      333    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   366 AA;  40782 MW;  11CCAD1F6091831B CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324


RESULT 4
1C04_GORGO
ID   1C04_GORGO     STANDARD;      PRT;   366 AA.
AC   P30387;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-APR-1993 (Rel. 25, Last annotation update)
DE   Class I histocompatibility antigen, GOGO-C0203 alpha chain precursor.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
```

```
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60248; CAA42800.1; -.
DR   PIR; JH0547; JH0547.
DR   HSSP; P30685; 1A9E.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    366       CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 GOGO-C0203 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    332
FT   DOMAIN      333    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   366 AA;  40970 MW;  EE962C8189CAC001 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324


RESULT 5
1C07_HUMAN
ID   1C07_HUMAN     STANDARD;      PRT;   366 AA.
AC   P10321; O78061; O78083; Q29631; Q29652; Q29867; Q29990; Q95463;
AC   Q95603; Q9MY31; Q9TQP9;
DT   01-MAR-1989 (Rel. 10, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   HLA class I histocompatibility antigen, Cw-7 alpha chain precursor
DE   (MHC class I antigen Cw*7).
GN   HLA-C OR HLAC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-206 FROM N.A. (CW*0701).
RX   MEDLINE=95176330; PubMed=7871529;
RA   Steinle A., Schendel D.J.;
RT   "HLA class I alleles of LCL 721 and 174xCEM.T2(T2).";
RL   Tissue Antigens 44:268-270(1994).
RN   [2]
RP   SEQUENCE OF 77-309 FROM N.A. (CW*0701).
RX   MEDLINE=89233295; PubMed=2714852;
RA   Pohla H., Kuon W., Tabaczewski P., Doerner C., Weiss E.H.;
RT   "Allelic variation in HLA-B and HLA-C sequences and the evolution of
RT   the HLA-B alleles.";
RL   Immunogenetics 29:297-307(1989).
RN   [3]
RP   SEQUENCE OF 26-338 FROM N.A. (CW*0701).
RX   MEDLINE=99416847; PubMed=10488744;
RA   van der Vlies S.A., Voorter C.E., van den Berg-Loonen E.M.;
RT   "There is more to HLA -C than exons 2 and 3: sequencing exons 1, 4 and
RT   5.";
RL   Tissue Antigens 54:169-177(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (CW*0702 AND CW*0704).
RC   TISSUE=Blood;
RX   MEDLINE=96232973; PubMed=8655361;
RA   Wang H., Tokunaga K., Ishikawa Y., Asahina A., Kuwata S., Akaza T.,
RA   Tadokoro K., Shibata Y., Takiguchi M., Juji T.;
RT   "Identification and DNA typing of two Cw7 alleles (Cw*0702 and
RT   Cw*0704) in Japanese, with the corrected sequence of Cw*0702.";
RL   Hum. Immunol. 45:52-58(1996).
RN   [5]
RP   SEQUENCE FROM N.A. (CW*0702).
RX   MEDLINE=98099755; PubMed=9435339;
RA   Cooper S.L., Adams E.J., Wells R.S., Walker C.M., Parham P.;
RT   "A major histocompatibility complex class I allele shared by two
RT   species of chimpanzee.";
RL   Immunogenetics 47:212-217(1998).
RN   [6]
RP   SEQUENCE FROM N.A. (CW*0702 AND CW*0704).
RC   TISSUE=Blood;
RX   MEDLINE=22512041; PubMed=12622774;
RA   Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RA   Madrigal J.A., Little A.-M.;
RT   "Cloning and sequencing full-length HLA-B and -C genes.";
RL   Tissue Antigens 61:20-48(2003).
RN   [7]
RP   SEQUENCE OF 25-366 FROM N.A. (CW*0703).
RX   MEDLINE=86033791; PubMed=3863816;
RA   Davidson W.F., Kress M., Khoury G., Jay G.;
RT   "Comparison of HLA class I gene sequences. Derivation of
RT   locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
RT   HLA-C genes.";
RL   J. Biol. Chem. 260:13414-13423(1985).
RN   [8]
RP   SEQUENCE FROM N.A. (CW*0704).
RX   MEDLINE=96086482; PubMed=7482492;
RA   Vilches C., Bunce M., de Pablo R., Herrero M.J., Kreisler M.;
RT   "Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by
RT   PCR-SSP.";
RL   Tissue Antigens 46:19-23(1995).
RN   [9]
RP   SEQUENCE FROM N.A. (CW*0704).
RC   TISSUE=Melanoma;
RA   Coulie P.G.;
RT   "Identification of a new HLA-Cw7 allele.";
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE FROM N.A. (CW*0706).
RX   MEDLINE=97161041; PubMed=9008313;
RA   Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;
RT   "Molecular cloning of two new HLA-C alleles: Cw*1801 and Cw*0706.";
RL   Tissue Antigens 48:698-702(1996).
RN   [11]
RP   SEQUENCE OF 26-206 FROM N.A. (CW*0709).
RX   MEDLINE=98349393; PubMed=9686604;
RA   Turner S., Ellexson M.E., Hickman H.D., Sidebottom D.A.,
RA   Fernandez-Vina M., Confer D.L., Hildebrand W.H.;
RT   "Sequence-based typing provides a new look at HLA-C diversity.";
RL   J. Immunol. 161:1406-1413(1998).
```

```
RN   [12]
RP   SEQUENCE FROM N.A. (CW*0711).
RX   MEDLINE=99299762; PubMed=10372547;
RA   Baurain J.-F., Coulie P.G.;
RT   "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";
RL   Tissue Antigens 53:510-512(1999).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- POLYMORPHISM: The following alleles of Cw-7 are known: Cw*0701,
CC       Cw*0702, Cw*0703, Cw*0704, Cw*0706, Cw*0709 and Cw*0711. The
CC       sequence shown is that of Cw*0701.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z46810; CAA86840.1; -.
DR   EMBL; M28207; AAA53259.1; -.
DR   EMBL; Y18533; CAB71800.1; -.
DR   EMBL; Y18534; CAB71800.1; JOINED.
DR   EMBL; Y18535; CAB71800.1; JOINED.
DR   EMBL; Y18536; CAB71800.1; JOINED.
DR   EMBL; D38526; BAA07531.1; -.
DR   EMBL; D49819; BAA08625.1; -.
DR   EMBL; D49552; BAA08500.1; -.
DR   EMBL; AJ001977; CAA05125.1; ALT_SEQ.
DR   EMBL; AJ293016; CAC04321.1; -.
DR   EMBL; AJ293017; CAC04322.1; -.
DR   EMBL; AJ291815; CAC19191.1; -.
DR   EMBL; M11886; AAA52665.1; -.
DR   EMBL; X83394; CAA58313.1; -.
DR   EMBL; U09853; AAA50217.1; -.
DR   EMBL; X97321; CAA65986.1; -.
DR   EMBL; AF015557; AAC17722.1; -.
DR   EMBL; AF015556; AAC17722.1; JOINED.
DR   EMBL; AJ010749; CAA09341.1; -.
DR   PIR; A24512; HLHUC4.
DR   PIR; I37078; I37078.
DR   PIR; I37529; I37529.
DR   PIR; I68750; I68750.
DR   HSSP; P30460; 1AGD.
DR   Genew; HGNC:4933; HLA-C.
DR   MIM; 142840; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT   SIGNAL        1     24
FT   CHAIN        25    366       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 CW-7 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    333
FT   DOMAIN      334    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   VARIANT      90     90       N -> K (in allele Cw*0702, allele
FT                                Cw*1703, allele Cw*0704 and allele
FT                                Cw*0711).
FT                                /FTId=VAR_016590.
FT   VARIANT     101    101       S -> N (in allele Cw*0709).
FT                                /FTId=VAR_016591.
FT   VARIANT     104    104       N -> K (in allele Cw*0709).
FT                                /FTId=VAR_016592.
FT   VARIANT     119    119       L -> P (in allele Cw*0704 and allele
FT                                Cw*0711).
FT                                /FTId=VAR_016593.
FT   VARIANT     123    123       Y -> S (in allele Cw*0702 and allele
FT                                Cw*0703).
FT                                /FTId=VAR_016594.
FT   VARIANT     140    140       S -> F (in allele Cw*0704 and allele
FT                                Cw*0711).
FT                                /FTId=VAR_016595.
FT   VARIANT     171    171       L -> W (in allele Cw*0703).
FT                                /FTId=VAR_016646.
FT   VARIANT     180    180       L -> D (in allele Cw*0704 and allele
FT                                Cw*0711).
FT                                /FTId=VAR_016596.
FT   VARIANT     187    187       T -> L (in allele Cw*0703).
FT                                /FTId=VAR_016647.
FT   VARIANT     201    201       E -> K (in allele Cw*0704 and allele
FT                                Cw0711).
FT                                /FTId=VAR_016597.
FT   VARIANT     331    331       M -> K (in allele Cw*0706).
FT                                /FTId=VAR_016598.
FT   VARIANT     348    348       A -> V (in allele Cw*0706).
FT                                /FTId=VAR_016599.
FT   VARIANT     363    363       T -> A (in allele Cw*0711).
FT                                /FTId=VAR_016600.
FT   CONFLICT     15     16       GG -> AA (IN REF. 8).
FT   CONFLICT     41     41       R -> A (IN REF. 8).

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324


RESULT 6
1C18_HUMAN
ID   1C18_HUMAN     STANDARD;      PRT;   366 AA.
AC   Q29865; O78203; P79498;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   HLA class I histocompatibility antigen, Cw-18 alpha chain precursor
DE   (MHC class I antigen Cw*18).
GN   HLA-C OR HLAC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (CW*1801).
RX   MEDLINE=97161041; PubMed=9008313;
RA   Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;
RT   "Molecular cloning of two new HLA-C alleles: Cw*1801 and Cw*0706.";
RL   Tissue Antigens 48:698-702(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (CW*1801).
RX   MEDLINE=22512041; PubMed=12622774;
RA   Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RA   Madrigal J.A., Little A.-M.;
RT   "Cloning and sequencing full-length HLA-B and -C genes.";
RL   Tissue Antigens 61:20-48(2003).
```

```
RN   [3]
RP   SEQUENCE OF 26-206 FROM N.A. (CW*1801).
RX   MEDLINE=98119594; PubMed=9459506;
RA   Grundschober C., Labonne M., Javaux P., Steiner Q.G., Gebuhrer L.,
RA   Tiercy J.M.;
RT   "Sequence of four new HLA-Cw alleles: a possible role of interallelic
RT   recombination.";
RL   Tissue Antigens 51:72-79(1998).
RN   [4]
RP   SEQUENCE FROM N.A. (CW*1802).
RX   MEDLINE=97378891; PubMed=9234488;
RA   Vilches C., Bunce M., de Pablo R., Moreno M.E., Puente S., Sanz L.,
RA   Kreisler M.;
RT   "The novel HLA-Cw*1802 allele is found associated with B*5703 in the
RT   Bubi population from Equatorial Guinea.";
RL   Tissue Antigens 49:644-649(1997).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- POLYMORPHISM: The following alleles of Cw-18 are known: Cw*1801
CC       (Cw*04GB) and Cw*1802 (Cw*18GB). The sequence shown is that of
CC       Cw*1801.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X96582; CAA65401.1; -.
DR   EMBL; AJ420253; CAD12438.1; -.
DR   EMBL; Z80227; CAB02408.1; -.
DR   EMBL; Y09156; CAA70354.1; -.
DR   HSSP; P30460; 1AGD.
DR   Genew; HGNC:4933; HLA-C.
DR   MIM; 142840; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT   SIGNAL       1    24
FT   CHAIN       25   366       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                               CW-18 ALPHA CHAIN.
FT   DOMAIN      25   114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN     115   206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN     207   298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN     299   308       CONNECTING PEPTIDE.
FT   TRANSMEM   309   333
FT   DOMAIN     334   366       CYTOPLASMIC TAIL.
FT   DISULFID   125   188       BY SIMILARITY.
FT   DISULFID   227   283       BY SIMILARITY.
FT   CARBOHYD   110   110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   VARIANT    319   319       V -> A (in allele Cw*1802).
FT                              /FTId=VAR_016635.
SQ   SEQUENCE   366 AA;  40933 MW;  67CE7E948E4327D8 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
                  ||||||||
Db        317 VLVVLAVL 324


RESULT 7
YGIK_SALTY
ID   YGIK_SALTY     STANDARD;      PRT;   435 AA.
AC   P40800;
DT   01-FEB-1995 (Rel. 31, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein ygiK.
GN   YGIK OR STM3171.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RA   Cong J., Schmid M.B.;
RL   Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (Probable).
CC   -!- SIMILARITY: BELONGS TO THE YIAN/YGIK FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U09309; AAA56680.1; -.
DR   EMBL; AE008845; AAL22045.1; -.
DR   StyGene; SG10523; ygiK.
DR   InterPro; IPR000252; DedA.
DR   InterPro; IPR004681; TRAP_transptDctM.
DR   Pfam; PF00597; DedA; 1.
DR   TIGRFAMs; TIGR00786; dctM; 1.
KW   Hypothetical protein; Transmembrane; Inner membrane;
KW   Complete proteome.
FT   TRANSMEM     9    29       POTENTIAL.
FT   TRANSMEM    57    77       POTENTIAL.
FT   TRANSMEM   110   130       POTENTIAL.
FT   TRANSMEM   146   166       POTENTIAL.
FT   TRANSMEM   176   196       POTENTIAL.
FT   TRANSMEM   226   246       POTENTIAL.
FT   TRANSMEM   280   300       POTENTIAL.
FT   TRANSMEM   321   341       POTENTIAL.
FT   TRANSMEM   343   363       POTENTIAL.
FT   TRANSMEM   367   387       POTENTIAL.
FT   TRANSMEM   408   428       POTENTIAL.
FT   CONFLICT   119   119       A -> R (IN REF. 1).
FT   CONFLICT   124   124       A -> P (IN REF. 1).
SQ   SEQUENCE   435 AA;  46004 MW;  EEA79EFCFEE8A58A CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        242 IGGIIGGV 249
              ||||||||
Db        236 IGGIIGGV 243


RESULT 8
TATB_STRCO
ID   TATB_STRCO     STANDARD;      PRT;   161 AA.
AC   Q9PBX8;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sec-independent protein translocase protein tatB homolog.
GN   TATB OR SCO5150 OR SCP8.13.
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
CC   -!- FUNCTION: Required for correct localization of precursor proteins
CC       bearing signal peptides with the twin arginine conserved motif
CC       S/T-R-R-X-F-L-K. This sec-independent pathway is termed TAT for
CC       twin-arginine translocation system. This system mainly transports
CC       proteins with bound cofactors that require folding prior to export
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
CC   -!- SIMILARITY: Belongs to the tatB family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AL939122; CAC01351.1; -.
DR   HAMAP; MF_00237; -; 1.
DR   InterPro; IPR003998; TatB.
DR   PRINTS; PR01506; TATBPROTEIN.
KW   Transport; Protein transport; Translocation; Transmembrane;
KW   Membrane; Complete proteome.
FT   TRANSMEM      2      22       POTENTIAL.
SQ   SEQUENCE   161 AA;  17757 MW;  0510C0D221BEEEF3 CRC64;

  Query Match              2.3%;  Score 7;  DB 1;  Length 161;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 LVVLAVL 256
              |||||||
Db         13 LVVLAVL 19


RESULT 9
XLR1_MOUSE
ID   XLR1_MOUSE     STANDARD;      PRT;   224 AA.
AC   Q9Z1L4;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Retinoschisin precursor (X-linked juvenile retinoschisis protein
DE   homolog).
GN   RS1 OR RS1H OR XLRS1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RX   MEDLINE=99160474; PubMed=10051329;
RA   Gehrig A.E., Warneke-Wittstock R., Sauer C.G., Weber B.H.F.;
RT   "Isolation and characterization of the murine X-linked juvenile
RT   retinoschisis (Rs1h) gene.";
RL   Mamm. Genome 10:303-307(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Brunner B., Todt T., Lenzner S., Stout K., Schulz U., Ropers H.-H.,
RA   Kalscheuer V.M.;
RT   "Genomic structure and comparative analysis of seven contiguous genes
RT   disclose a large region with conserved gene order in human Xp22.2-
RT   p22.1.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=99148018; PubMed=10023077;
RA   Reid S.N., Akhmedov N.B., Piriev N.I., Kozak C.A., Danciger M.,
RA   Farber D.B.;
RT   "The mouse X-linked juvenile retinoschisis cDNA: expression in
RT   photoreceptors.";
RL   Gene 227:257-266(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May be active in cell adhesion processes during retinal
CC       development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- TISSUE SPECIFICITY: Retinal specific.
CC   -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF084561; AAD21808.1; -.
DR   EMBL; AF084567; AAD21809.1; -.
DR   EMBL; AF084562; AAD21809.1; JOINED.
DR   EMBL; AF084563; AAD21809.1; JOINED.
DR   EMBL; AF084564; AAD21809.1; JOINED.
DR   EMBL; AF084565; AAD21809.1; JOINED.
DR   EMBL; AF084566; AAD21809.1; JOINED.
DR   EMBL; AJ011381; CAA09601.1; -.
DR   EMBL; BC046422; AAH46422.1; -.
DR   HSSP; P12259; 1CZT.
DR   MGD; MGI:1336189; Rs1h.
DR   InterPro; IPR000421; FA58_C.
DR   InterPro; IPR008979; Gal_bind_like.
DR   Pfam; PF00754; F5_F8_type_C; 1.
DR   SMART; SM00231; FA58C; 1.
DR   PROSITE; PS01285; FA58C_1; 1.
DR   PROSITE; PS01286; FA58C_2; FALSE_NEG.
DR   PROSITE; PS50022; FA58C_3; 1.
KW   Cell adhesion; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    224       RETINOSCHISIN.
FT   DOMAIN       63    219       F5/8 TYPE C.
FT   DISULFID     63    219       BY SIMILARITY.
SQ   SEQUENCE   224 AA;  25575 MW;  4536203CC00E90E4 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 PFLLLLP 24
              |||||||
Db          8 PFLLLLP 14


RESULT 10
RS2_SHEON
ID   RS2_SHEON      STANDARD;      PRT;   242 AA.
AC   Q8EGH5;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   30S ribosomal protein S2.
GN   RPSB OR SO1629.
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Alteromonadaceae; Shewanella.
OX   NCBI_TaxID=70863;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MR-1;
RX   MEDLINE=22297686; PubMed=12368813;
RA   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA   Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA   Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA   Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA   Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA   Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis.";
RL   Nat. Biotechnol. 20:1118-1123(2002).
CC   -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE015609; AAN54684.1; -.
DR   TIGR; SO1629; -.
DR   HAMAP; MF_00291; -; 1.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   InterPro; IPR005706; Ribosomal_S2_b/o.
DR   Pfam; PF00318; Ribosomal_S2; 1.
DR   PRINTS; PR00395; RIBOSOMALS2.
DR   TIGRFAMs; TIGR01011; rpsB_bact; 1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR   PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE   242 AA;  26569 MW;  74AA24550750B88C CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        288 PDGVNYI 294
              |||||||
Db        193 PDGVNYI 199


RESULT 11
TNFC_HUMAN
ID   TNFC_HUMAN     STANDARD;      PRT;   244 AA.
AC   Q06643; P78370; Q99761;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   LTB OR TNFSF3 OR TNFC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RC   TISSUE=T-cell;
RX   MEDLINE=93208881; PubMed=7916655;
RA   Browning J.L., Ngam-Ek A., Lawton P., Demarinis J., Tizard R.,
RA   Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT   "Lymphotoxin beta, a novel member of the TNF family that forms a
RT   heteromeric complex with lymphotoxin on the cell surface.";
RL   Cell 72:847-856(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=97445965; PubMed=9299492;
RA   Warzocha K., Renard N., Charlot C., Bienvenu J., Coiffier B.,
RA   Salles G.;
RT   "Identification of two lymphotoxin beta isoforms expressed in human
RT   lymphoid cell lines and non-Hodgkin's lymphomas.";
RL   Biochem. Biophys. Res. Commun. 238:273-276(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Neville M.J., Milner C.M., Campbell R.D.;
RT   "A new member of the immunoglobulin superfamily and a V-ATPase G
RT   subunit are amongst the predicted products of novel genes close to the
RT   TNF locus in the human MHC.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA   Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA   Lasky S., Hood L.;
RT   "Sequence of the human major histocompatibility complex class III
RT   region.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Shiina S., Tamiya G., Oka A., Inoko H.;
RT   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
```

```
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-70 AND
RP   PRO-111.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS ARG-84 AND PHE-87.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface. Isoform 2 is probably non-functional.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) one LTB and two LTA subunits.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q06643-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06643-2; Sequence=VSP_006441, VSP_006442;
CC   -!- TISSUE SPECIFICITY: Spleen and thymus.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L11016; AAA99888.1; -.
DR   EMBL; U89922; AAC51769.1; -.
DR   EMBL; U79029; AAB37342.1; -.
DR   EMBL; L11015; AAA36191.1; -.
DR   EMBL; Y14768; CAA75069.1; -.
DR   EMBL; AP129756; AAD18089.1; -.
DR   EMBL; AP000505; BAB63395.1; -.
DR   EMBL; AY070219; AAL49954.1; -.
DR   EMBL; AY070219; AAL49955.1; -.
DR   EMBL; AY216497; AAO21134.1; -.
DR   PIR; A46066; A46066.
DR   PIR; JC5645; JC5645.
DR   HSSP; P01374; 1TNR.
DR   Genew; HGNC:6711; LTB.
DR   MIM; 600978; -.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0015070; F:toxin activity; NAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW   Alternative splicing; Polymorphism.
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      19    48       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN        49    244      EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD      222   222      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      53    77       GLVTETADPGAQAQQGLGFQKLPEE -> GLGFRSCQRRSQ
FT                                KQISAPGSQLPTS (in isoform 2).
FT                                /FTId=VSP_006441.
FT   VARSPLIC      78    244      Missing (in isoform 2).
FT                                /FTId=VSP_006442.
FT   VARIANT       70    70       G -> E.
FT                                /FTId=VAR_013025.
FT   VARIANT       84    84       S -> R.
FT                                /FTId=VAR_016331.
FT   VARIANT       87    87       L -> P.
FT                                /FTId=VAR_016332.
FT   VARIANT       111   111      A -> P.
FT                                /FTId=VAR_013026.
FT   CONFLICT      60    69       DPGAQAQQGL -> GLSAPGSGRT (IN REF. 2;
FT                                AAB37342).
SQ   SEQUENCE   244 AA;  25390 MW;  F415694598308ED4C CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLAVLAL 258
              |||||||
Db         40 VLAVLAL 46


RESULT 12
TNFC_PANTR
ID   TNFC_PANTR     STANDARD;      PRT;   244 AA.
AC   Q862Z7;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   LTB OR TNFSF3 OR TNFC.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22381002; PubMed=12493009;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22709134; PubMed=12799463;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Pujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface (By similarity).
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AB054536; BAB83881.1; -.
DR   EMBL; AB100082; BAC78156.1; -.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     48       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       49    244       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   244 AA;  25420 MW;  A4047858335D5B97 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLAVLAL 258
              |||||||
Db         40 VLAVLAL 46


RESULT 13
HTPX_AQUAE
ID   HTPX_AQUAE     STANDARD;      PRT;   302 AA.
AC   O67798;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Probable protease htpX homolog (EC 3.4.24.-).
GN   HTPX OR AQ_1991.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to peptidase family M48.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AE000766; AAC07747.1; -.
DR   PIR; B70471; B70471.
DR   MEROPS; M48.004; -.
DR   HAMAP; MF_00188; -; 1.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001915; Peptidase_M48.
DR   Pfam; PF01435; Peptidase_M48; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW   Transmembrane; Hydrolase; Metalloprotease; Zinc; Complete proteome.
FT   TRANSMEM     27     47       POTENTIAL.
FT   TRANSMEM    151    171       POTENTIAL.
FT   TRANSMEM    195    215       POTENTIAL.
FT   METAL       141    141       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    142    142       BY SIMILARITY.
FT   METAL       145    145       ZINC (CATALYTIC) (BY SIMILARITY).
SQ   SEQUENCE   302 AA;  33030 MW;  3278BF481568E895 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 302;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        242 IGGIIGG 248
              |||||||
Db         31 IGGIIGG 37


RESULT 14
TNFC_MOUSE
ID   TNFC_MOUSE     STANDARD;      PRT;   306 AA.
AC   P41155;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   LTB OR TNFSF3 OR TNFC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=95148600; PubMed=7846035;
RA   Pokholok D.K., Maroulakou I.G., Kuprash D.V., Alimzhanov M.B.,
RA   Kozlov S.V., Novobrantseva T.I., Turetskaya R.L., Green J.E.,
RA   Nedospasov S.A.;
RT   "Cloning and expression analysis of the murine lymphotoxin beta
RT   gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:674-678(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=95088371; PubMed=7995944;
RA   Lawton P., Nelson J., Tizard R., Browning J.L.;
RT   "Characterization of the mouse lymphotoxin-beta gene.";
RL   J. Immunol. 154:239-246(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA   Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RT   "Sequence of the mouse major histocompatibility class III region.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; U12029; AAA67716.1; -.
```

```
DR   EMBL; U16984; AAB60493.1; -.
DR   EMBL; U16985; AAA70089.1; -.
DR   EMBL; U06950; AAA18592.1; -.
DR   EMBL; AF109719; AAC82483.1; -.
DR   PIR; I49139; I49139.
DR   MGD; MGI:104796; Ltb.
DR   GO; GO:0007515; P:lymph gland development; IMP.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT   DOMAIN       1     27       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     28    48       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN       49    306      EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     98    98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     284   284      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   306 AA;  32328 MW;  B7D276AB84A22549 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLAVLAL 258
              |||||||
Db         40 VLAVLAL 46


RESULT 15
TNFC_MARMO
ID   TNFC_MARMO     STANDARD;      PRT;   310 AA.
AC   Q9JM10; Q9JM11;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   LTB OR TNFSF3 OR TNFC.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20184748; PubMed=10721723;
RA   Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT   "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT   structure, characterization and biological activity.";
RL   Gene 242:295-305(2000).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF096268; AAF34866.1; -.
DR   EMBL; AF095587; AAF34865.1; -.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT   DOMAIN       1     27       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     28    48       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN       49    310      EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     272   272      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     280   280      D -> H (IN REF. 1; AAF34865).
SQ   SEQUENCE   310 AA;  32644 MW;  73B354EFC8B3B3BE CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 VLAVLAL 258
              |||||||
Db         40 VLAVLAL 46


Search completed: June 15, 2004, 11:10:31
Job time : 11 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:50 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	310	100.0	310	4	Q9BX67	Q9bx67 homo sapien
2	310	100.0	355	4	Q8WWL8	Q8wwl8 homo sapien
3	208	67.1	309	4	Q96FL1	Q96fl1 homo sapien
4	32	10.3	310	11	Q9D8B7	Q9d8b7 mus musculu
5	28	9.0	310	11	Q9D1M9	Q9d1m9 mus musculu
6	28	9.0	310	11	Q9EPK4	Q9epk4 mus musculu
7	13	4.2	64	11	Q8BT59	Q8bt59 mus musculu
8	8	2.6	39	7	Q9TNT2	Q9tnt2 homo sapien
9	8	2.6	67	7	Q8HWG1	Q8hwg1 homo sapien
10	8	2.6	76	5	Q867W1	Q867w1 procambarus
11	8	2.6	131	5	Q8I8S1	Q8i8s1 anopheles g
12	8	2.6	154	11	Q8C4V2	Q8c4v2 mus musculu
13	8	2.6	231	16	Q89E35	Q89e35 bradyrhizob
14	8	2.6	231	17	Q8TQT5	Q8tqt5 methanosarc
15	8	2.6	232	17	Q8ZSR8	Q8zsr8 pyrobaculum
16	8	2.6	233	10	Q9LR49	Q9lr49 arabidopsis
17	8	2.6	246	5	Q966C0	Q966c0 caenorhabdi
18	8	2.6	294	16	Q98EQ9	Q98eq9 rhizobium l
19	8	2.6	309	5	Q9N4Y9	Q9n4y9 caenorhabdi
20	8	2.6	322	2	Q9RPI7	Q9rpi7 desulfitoba
21	8	2.6	336	10	Q9C7E9	Q9c7e9 arabidopsis
22	8	2.6	338	7	Q9MXL5	Q9mxl5 pan troglod
23	8	2.6	348	7	Q9MWJ9	Q9mwj9 gorilla gor
24	8	2.6	348	16	Q9PR46	Q9pr46 ureaplasma
25	8	2.6	363	7	Q95HC2	Q95hc2 homo sapien
26	8	2.6	365	7	Q9XRX8	Q9xrx8 pongo pygma
27	8	2.6	365	7	Q9XRX7	Q9xrx7 pongo pygma
28	8	2.6	365	7	Q9MXG4	Q9mxg4 pan troglod
29	8	2.6	366	6	O46684	O46684 pan troglod
30	8	2.6	366	7	Q8MHH0	Q8mhh0 pongo pygma
31	8	2.6	366	7	Q8MHH1	Q8mhh1 pongo pygma
32	8	2.6	366	7	Q8MHG8	Q8mhg8 pongo pygma
33	8	2.6	366	7	Q8MHG9	Q8mhg9 pongo pygma
34	8	2.6	366	7	O19617	O19617 homo sapien
35	8	2.6	366	7	Q860B0	Q860b0 homo sapien
36	8	2.6	366	7	Q85ZX8	Q85zx8 homo sapien
37	8	2.6	366	7	Q9TPL2	Q9tpl2 pan troglod
38	8	2.6	366	7	Q9MXD2	Q9mxd2 pan troglod
39	8	2.6	366	7	Q7YQB2	Q7yqb2 homo sapien
40	8	2.6	449	16	Q8CWZ7	Q8cwz7 streptococc
41	8	2.6	452	16	Q8G5D2	Q8g5d2 bifidobacte
42	8	2.6	492	16	Q8Z1U9	Q8z1u9 salmonella
43	8	2.6	659	16	Q8EK37	Q8ek37 shewanella
44	8	2.6	784	16	Q9CIF4	Q9cif4 lactococcus
45	8	2.6	1290	13	Q9W6E1	Q9w6e1 gallus gall

ALIGNMENTS

RESULT 1
Q9BX67
ID Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion
DE molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesional Molecule-3 on Human
RT Platelets: A New Member of Immunoglobulin Superfamily.";

```
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   EMBL; AF448478; AAM20925.1; -.
DR   EMBL; AK074769; BAC11195.1; -.
DR   EMBL; AK075309; BAC11538.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;

  Query Match             100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
Q8WWL8
ID   Q8WWL8      PRELIMINARY;      PRT;   355 AA.
AC   Q8WWL8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule 3.
GN   JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hearn T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Phillips H.M.;
RT   "Narrowing the critical region within 11q24-qter for hypoplastic left
RT   heart and identification of a candidate gene, JAM3, expressed during
RT   cardiogenesis.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416101; CAC94776.1; -.
DR   Genew; HGNC:15532; JAM3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   CHAIN        76    355       JUNCTION ADHESION MOLECULE 3.
SQ   SEQUENCE   355 AA;  39602 MW;  8B1577DEA7B1D4F8 CRC64;

  Query Match             100.0%;  Score 310;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 105

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 165

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 225

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 285

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 345

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        346 DFRHKSSFVI 355


RESULT 3
Q96FL1
ID   Q96FL1      PRELIMINARY;      PRT;   309 AA.
AC   Q96FL1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010690; AAH10690.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
FT   NON_TER      1     1
SQ   SEQUENCE   309 AA;  34917 MW;  50C5B1B7872E8DF3 CRC64;

  Query Match             67.1%;  Score 208;  DB 4;  Length 309;
  Best Local Similarity   99.7%;  Pred. No. 7.5e-212;
  Matches  308;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          2 ALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTS 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEPESVELSCIITDSQTS 60

Qy         62 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 120

Qy        122 DRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 181
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 180

Qy        182 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240

Qy        242 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 300

Qy        302 FRHKSSFVI 310
              |||||||||
Db        301 FRHKSSFVI 309
```

RESULT 4
Q9D8B7
ID Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 10.3%; Score 32; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         41 PVVQEPESVELSCIITDSQTSDPRIEWKKIQD 72
              ||||||||||||||||||||||||||||||||
Db         41 PVVQEPESVELSCIITDSQTSDPRIEWKKIQD 72
```

RESULT 5
Q9D1M9
ID Q9D1M9 PRELIMINARY; PRT; 310 AA.
AC Q9D1M9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003326; BAB22715.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 9.0%; Score 28; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         45 EPESVELSCIITDSQTSDPRIEWKKIQD 72
              ||||||||||||||||||||||||||||
Db         45 EPESVELSCIITDSQTSDPRIEWKKIQD 72
```

RESULT 6
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS Mus musculus (Mouse).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11036763;
RA   Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT   Family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   EMBL; BC024357; AAH24357.1; -.
DR   EMBL; AK032833; BAC28049.1; -.
DR   MGD; MGI:1933825; Jam3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;

  Query Match             9.0%;  Score 28;  DB 11;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-21;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         45 EFESVELSCIITDSQTSDPRIEWKKIQD 72
              ||||||||||||||||||||||||||||
Db         45 EFESVELSCIITDSQTSDPRIEWKKIQD 72


RESULT 7
Q8BT59
ID   Q8BT59      PRELIMINARY;      PRT;    64 AA.
AC   Q8BT59;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Junction cell adhesion molecule 3 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUB=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK017692; BAC25526.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   64 AA;  6996 MW;  AF46BC30AA6D0C11 CRC64;

  Query Match             4.2%;  Score 13;  DB 11;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        298 EEGDFRHKSSFVI 310
              |||||||||||||
Db         52 EEGDFRHKSSFVI 64


RESULT 8
Q9TNT2
ID   Q9TNT2      PRELIMINARY;      PRT;    39 AA.
AC   Q9TNT2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MHC class I HLA C antigen (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RX   MEDLINE=99110146; PubMed=9894855;
RA   van der Vlies S., Voorter C., van den Berg-Loonen E.;
RT   "A reliable and efficient high resolution typing method for HLA C
RT   using sequence-based typing.";
RL   Tissue Antigens 52:558-568(1998).
DR   EMBL; Y16418; CAA76206.1; -.
KW   MHC.
FT   NON_TER       1      1
FT   NON_TER      39     39
SQ   SEQUENCE   39 AA;  3938 MW;  24613855AD783823 CRC64;

  Query Match             2.6%;  Score 8;  DB 7;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db         18 VLVVLAVL 25


RESULT 9
Q8HWG1
ID   Q8HWG1      PRELIMINARY;      PRT;    67 AA.
AC   Q8HWG1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
```

```
DE   MHC class I antigen (Fragment).
GN   HLA-CW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-17 FROM N.A.
RA   Delfino L., Morabito A., Ferrara G.B.;
RT   "HLA-Cw*07012 sequence updating: from exon 6 to exon 8.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY162385; AAN84536.1; -.
DR   EMBL; AY162382; AAN84536.1; JOINED.
DR   EMBL; AY162383; AAN84536.1; JOINED.
DR   EMBL; AY162384; AAN84536.1; JOINED.
FT   NON_TER       1       1
SQ   SEQUENCE   67 AA;  6538 MW;  543B57F5F97D7FF1 CRC64;

  Query Match             2.6%;  Score 8;  DB 7;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db         18 VLVVLAVL 25


RESULT 10
Q867W1
ID   Q867W1      PRELIMINARY;      PRT;    76 AA.
AC   Q867W1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide precursor protein.
OS   Procambarus clarkii (Red swamp crayfish).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Astacoidea; Cambaridae; Procambarus.
OX   NCBI_TaxID=6728;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yasuda-Kamatani Y., Yasuda A.;
RT   "Cloning of cDNA for a neuropeptide precursor protein from Procambarus
RT   clarkii.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB036712; BAC55939.1; -.
DR   EMBL; AB036713; BAC55940.1; -.
SQ   SEQUENCE   76 AA;  7895 MW;  3A3DF225947483AA CRC64;

  Query Match             2.6%;  Score 8;  DB 5;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db         14 VLVVLAVL 21


RESULT 11
Q8I8S1
ID   Q8I8S1      PRELIMINARY;      PRT;   131 AA.
AC   Q8I8S1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Odorant-binding protein G.38B.a.
OS   Anopheles gambiae (African malaria mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=7165;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Xu P., Smith D.P.;
RT   "Identification of distinct families of odorant-binding in the genome
RT   of Anopheles gambiae.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY146730; AAO12090.1; -.
DR   GO; GO:0005549; F:odorant binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR006170; PBP_GOBP.
DR   Pfam; PF01395; PBP_GOBP; 1.
SQ   SEQUENCE   131 AA;  14884 MW;  FC7D52E9740E2A64 CRC64;

  Query Match             2.6%;  Score 8;  DB 5;  Length 131;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        246 IGGVLVVL 253
              ||||||||
Db          7 IGGVLVVL 14


RESULT 12
Q8C4V2
ID   Q8C4V2      PRELIMINARY;      PRT;   154 AA.
AC   Q8C4V2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK080981; BAC38104.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   154 AA;  17098 MW;  F032A4B8C5483EC6 CRC64;

  Query Match             2.6%;  Score 8;  DB 11;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        224 DAGSARCE 231
              ||||||||
Db         72 DAGSARCE 79


RESULT 13
Q89E35
ID   Q89E35      PRELIMINARY;      PRT;   231 AA.
AC   Q89E35;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bll7252 protein.
GN   BLL7252.
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA 110;
RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
```

```
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
DR   EMBL; AP005961; BAC52517.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR004254; HlyIII_related.
DR   Pfam; PF03006; UPF0073; 1.
KW   Complete proteome.
SQ   SEQUENCE   231 AA;  25052 MW;  254EB5B98D40D58B CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db         50 VLVVLAVL 57


RESULT 14
Q8TQT5
ID   Q8TQT5      PRELIMINARY;      PRT;   231 AA.
AC   Q8TQT5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cell surface lipoprotein.
GN   MA1454.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC   Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010815; AAM04868.1; -.
DR   InterPro; IPR008972; Cupredoxin.
KW   Lipoprotein; Complete proteome.
SQ   SEQUENCE   231 AA;  25437 MW;  7AAB21CEE0B6500B CRC64;

  Query Match             2.6%;  Score 8;  DB 17;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 LVVLAVLA 257
              ||||||||
Db         23 LVVLAVLA 30


RESULT 15
Q8ZSR8
ID   Q8ZSR8      PRELIMINARY;      PRT;   232 AA.
AC   Q8ZSR8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein PAE3614.
GN   PAE3614.
OS   Pyrobaculum aerophilum.
OC   Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC   Thermoproteaceae; Pyrobaculum.
OX   NCBI_TaxID=13773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX   MEDLINE=21664397; PubMed=11792869;
RA   Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA   Miller J.H.;
RT   "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT   aerophilum.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR   EMBL; AE009941; AAL65045.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   232 AA;  25942 MW;  39A5BECC4403F903 CRC64;

  Query Match             2.6%;  Score 8;  DB 17;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 DFFLLLLF 24
              ||||||||
Db          2 DFFLLLLF 9


Search completed: June 15, 2004, 11:11:56
Job time : 37 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1637	100.0	310	4	US-09-907-794A-423	Sequence 423, App
2	1637	100.0	310	4	US-09-905-125A-423	Sequence 423, App
3	1637	100.0	310	4	US-09-902-775A-423	Sequence 423, App
4	481	29.4	298	4	US-09-152-060-76	Sequence 76, Appl
5	461.5	28.2	312	4	US-09-254-465A-9	Sequence 9, Appli
6	461.5	28.2	312	4	US-09-907-794A-64	Sequence 64, Appl
7	461.5	28.2	312	4	US-09-905-125A-64	Sequence 64, Appl
8	461.5	28.2	312	4	US-09-902-775A-64	Sequence 64, Appl
9	457.5	27.9	300	4	US-09-254-465A-10	Sequence 10, Appl
10	424	25.9	299	3	US-09-188-930-331	Sequence 331, App
11	424	25.9	299	4	US-09-462-270-2	Sequence 2, Appli
12	424	25.9	299	4	US-09-254-465A-1	Sequence 1, Appli
13	424	25.9	299	4	US-09-312-283C-189	Sequence 189, App
14	424	25.9	299	4	US-09-312-283C-331	Sequence 331, App
15	424	25.9	299	4	US-09-907-794A-119	Sequence 119, App
16	424	25.9	299	4	US-09-905-125A-119	Sequence 119, App
17	424	25.9	299	4	US-09-902-775A-119	Sequence 119, App
18	412	25.2	299	3	US-09-188-930-189	Sequence 189, App
19	392.5	24.0	260	4	US-09-254-465A-23	Sequence 23, Appl
20	392.5	24.0	263	4	US-09-254-465A-25	Sequence 25, Appl
21	288	17.6	205	4	US-09-462-270-4	Sequence 4, Appli
22	228.5	14.0	319	1	US-08-597-495B-22	Sequence 22, Appl
23	228.5	14.0	319	3	US-09-068-051A-22	Sequence 22, Appl
24	228.5	14.0	319	4	US-09-336-536-67	Sequence 67, Appl
25	228.5	14.0	319	4	US-09-254-465A-6	Sequence 6, Appli
26	217.5	13.3	270	4	US-09-254-465A-24	Sequence 24, Appl
27	217.5	13.3	273	4	US-09-254-465A-26	Sequence 26, Appl
28	215.5	13.2	318	3	US-09-068-051A-32	Sequence 32, Appl
29	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
30	173.5	10.6	370	4	US-09-336-536-28	Sequence 28, Appl
31	171.5	10.5	394	4	US-09-336-536-39	Sequence 39, Appl
32	169.5	10.4	390	2	US-08-979-424-1	Sequence 1, Appli
33	169.5	10.4	390	4	US-09-907-794A-39	Sequence 39, Appl
34	169.5	10.4	390	4	US-09-905-125A-39	Sequence 39, Appl
35	169.5	10.4	390	4	US-09-902-775A-39	Sequence 39, Appl
36	167	10.2	365	4	US-09-336-536-40	Sequence 40, Appl
37	166.5	10.2	341	4	US-09-336-536-29	Sequence 29, Appl
38	163.5	10.0	398	4	US-09-778-510-6	Sequence 6, Appli
39	163.5	10.0	398	4	US-09-907-794A-84	Sequence 84, Appl
40	163.5	10.0	398	4	US-09-905-125A-84	Sequence 84, Appl
41	163.5	10.0	398	4	US-09-902-775A-84	Sequence 84, Appl
42	162.5	9.9	246	4	US-09-336-536-31	Sequence 31, Appl
43	161	9.8	313	4	US-09-700-397-4	Sequence 4, Appli
44	161	9.8	344	4	US-09-700-397-3	Sequence 3, Appli
45	160.5	9.8	365	3	US-08-928-383B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
```